

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : A61K 39/00, 39/29, C07K 7/00, 14/02, 14/82		A1	(11) International Publication Number: WO 99/45954 (43) International Publication Date: 16 September 1999 (16.09.99)
(21) International Application Number: PCT/US98/05039 (22) International Filing Date: 13 March 1998 (13.03.98)		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(71) Applicant: EPIMMUNE, INC. [US/US]; Suite 200, 655 Nancy Ridge Drive, San Diego, CA 92121 (US).		Published <i>With international search report.</i>	
(72) Inventors: SETTE, Alessandro; 5551 Linda Rosa Avenue, La Jolla, CA 92037 (US). KUBO, Ralph, T.; 12635 Futura Street, San Diego, CA 92130 (US). SIDNEY, John; 8541 D. Villa La Jolla Drive, La Jolla, CA 92037 (US). CELIS, Esteban; 13644 Landfair Road, San Diego, CA 92130 (US). GREY, Howard, M.; 9066 La Jolla Street, La Jolla, CA 92037 (US). SOUTHWOOD, Scott; 10679 Strathmore Drive, Santee, CA 92071 (US).			
(74) Agents: BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two embarcadero Center, San Francisco, CA 94111-3834 (US).			
(54) Title: HLA-BINDING PEPTIDES AND THEIR USES			
(57) Abstract			
<p>The present invention provides the means and methods for selecting immunogenic peptides and the immunogenic peptide compositions capable of specifically binding glycoproteins encoded by HLA allele and inducing T cell activation in T cells restricted by the allele. The peptides are useful to elicit an immune response against a desired antigen.</p>			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NB	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

HLA BINDING PEPTIDES AND THEIR USES

BACKGROUND OF THE INVENTION

The present invention relates to compositions and methods for preventing, treating or diagnosing a number of pathological states such as viral diseases and cancers.

5 In particular, it provides novel peptides capable of binding selected major histocompatibility complex (MHC) molecules and inducing an immune response.

MHC molecules are classified as either Class I or Class II molecules. Class II MHC molecules are expressed primarily on cells involved in initiating and sustaining immune responses, such as T lymphocytes, B lymphocytes, macrophages, etc. Class II 10 MHC molecules are recognized by helper T lymphocytes and induce proliferation of helper T lymphocytes and amplification of the immune response to the particular immunogenic peptide that is displayed. Class I MHC molecules are expressed on almost all nucleated cells and are recognized by cytotoxic T lymphocytes (CTLs), which then destroy the antigen-bearing cells. CTLs are particularly important in tumor rejection and 15 in fighting viral infections.

The CTL recognizes the antigen in the form of a peptide fragment bound to the MHC class I molecules rather than the intact foreign antigen itself. The antigen must normally be endogenously synthesized by the cell, and a portion of the protein antigen is degraded into small peptide fragments in the cytoplasm. Some of these small peptides 20 translocate into a pre-Golgi compartment and interact with class I heavy chains to facilitate proper folding and association with the subunit $\beta 2$ microglobulin. The peptide-MHC class I complex is then routed to the cell surface for expression and potential recognition by specific CTLs.

25 Investigations of the crystal structure of the human MHC class I molecule, HLA-A2.1, indicate that a peptide binding groove is created by the folding of the $\alpha 1$ and $\alpha 2$ domains of the class I heavy chain (Bjorkman et al., *Nature* 329:506 (1987)). In these investigations, however, the identity of peptides bound to the groove was not determined.

Buus et al., *Science* 242:1065 (1988) first described a method for acid elution of bound peptides from MHC. Subsequently, Rammensee and his coworkers (Falk

et al., Nature 351:290 (1991) have developed an approach to characterize naturally processed peptides bound to class I molecules. Other investigators have successfully achieved direct amino acid sequencing of the more abundant peptides in various HPLC fractions by conventional automated sequencing of peptides eluted from class I molecules of the B type (Jardetzky, et al., Nature 353:326 (1991) and of the A2.1 type by mass spectrometry (Hunt, et al., Science 225:1261 (1992). A review of the characterization of naturally processed peptides in MHC Class I has been presented by Rötzschke and Falk (Rötzschke and Falk, Immunol. Today 12:447 (1991).

Sette et al., Proc. Natl. Acad. Sci. USA 86:3296 (1989) showed that MHC 10 allele specific motifs could be used to predict MHC binding capacity. Schaeffer et al., Proc. Natl. Acad. Sci. USA 86:4649 (1989) showed that MHC binding was related to immunogenicity. Several authors (De Bruijn et al., Eur. J. Immunol., 21:2963-2970 (1991); Pamer et al., 991 Nature 353:852-955 (1991)) have provided preliminary evidence 15 that class I binding motifs can be applied to the identification of potential immunogenic peptides in animal models. Class I motifs specific for a number of human alleles of a given class I isotype have yet to be described. It is desirable that the combined frequencies of these different alleles should be high enough to cover a large fraction or perhaps the majority of the human outbred population.

Despite the developments in the art, the prior art has yet to provide a useful 20 human peptide-based vaccine or therapeutic agent based on this work. The present invention provides these and other advantages.

SUMMARY OF THE INVENTION

The present invention provides compositions comprising immunogenic peptides having binding motifs for HLA molecules. The immunogenic peptides, which bind to the appropriate MHC allele, comprise conserved residues at certain positions which allow the peptides to bind desired HLA molecules.

Epitopes on a number of immunogenic target proteins can be identified 30 using the peptides of the invention. Examples of suitable antigens include prostate cancer specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency type-1 virus (HIV1), Kaposi's sarcoma herpes virus (KSHV), human papilloma virus (HPV) antigens, Lassa

virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu. The peptides are thus useful in pharmaceutical compositions for both therapeutic and diagnostic applications.

In particular, the invention provides compositions comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14. Also provided are peptides comprising a conservative substitution of a residue in a peptide shown in Table 3-14. The immunogenic peptide of the invention can be further linked to a second oligopeptide. In some embodiments, the second oligopeptide is a peptide that induces a helper T response.

The invention further provides nucleic acid molecules encoding immunogenic peptides as shown in Tables 3-14, or peptides comprising a conservative substitution of a residue of a peptide shown in Table 3-14. The nucleic acid may further comprise a sequence encoding a second immunogenic peptide or peptide that induces a helper T response.

The peptides provided here can be used to induce a cytotoxic T cell response either *in vivo* or *in vitro*. The methods comprise contacting a cytotoxic T cell with a peptide of the invention.

Definitions

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of adjacent amino acids. The oligopeptides of the invention are less than about 15 residues in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues.

An "immunogenic peptide" is a peptide which comprises an allele-specific motif such that the peptide will bind an MHC molecule and induce a CTL response. Immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and inducing a cytotoxic T cell response against the antigen from which the immunogenic peptide is derived.

Immunogenic peptides are conveniently identified using the algorithms of the invention. The algorithms are mathematical procedures that produce a score which

enables the selection of immunogenic peptides. Typically one uses the algorithmic score with a "binding threshold" to enable selection of peptides that have a high probability of binding at a certain affinity and will in turn be immunogenic. The algorithm is based upon either the effects on MHC binding of a particular amino acid at a particular position of a peptide or the effects on binding of a particular substitution in a motif containing peptide.

5

A "conserved residue" is an amino acid which occurs in a significantly higher frequency than would be expected by random distribution at a particular position in a peptide. Typically a conserved residue is one where the MHC structure may provide a contact point with the immunogenic peptide. At least one to three or more, preferably two, conserved residues within a peptide of defined length defines a motif for an immunogenic peptide. These residues are typically in close contact with the peptide binding groove, with their side chains buried in specific pockets of the groove itself. Typically, an immunogenic peptide will comprise up to three conserved residues, more usually two conserved residues.

15

As used herein, "negative binding residues" are amino acids which if present at certain positions will result in a peptide being a nonbinder or poor binder and in turn fail to be immunogenic i.e. induce a CTL response.

20

The term "motif" refers to the pattern of residues in a peptide of defined length, usually about 8 to about 11 amino acids, which is recognized by a particular MHC allele. The peptide motifs are typically different for each human MHC allele and differ in the pattern of the highly conserved residues and negative residues.

The binding motif for an allele can be defined with increasing degrees of precision. In one case, all of the conserved residues are present in the correct positions in a peptide and there are no negative residues in positions 1,3 and/or 7.

25

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany it as found in its native state. Thus, the peptides of this invention do not contain materials normally associated with their *in situ* environment, e.g., MHC I molecules on antigen presenting cells. Even where a protein has been isolated to a homogenous or dominant band, there are trace contaminants in the range of 5-10% of native protein which co-purify with the desired protein. Isolated peptides of this invention do not contain such endogenous co-purified protein.

The term "residue" refers to an amino acid or amino acid mimetic incorporated in an oligopeptide by an amide bond or amide bond mimetic.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention relates to the determination of allele-specific peptide motifs for human Class I MHC (sometimes referred to as HLA) allele subtypes, in particular, peptide motifs recognized by HLA alleles.

For HLA-A2.1 alleles a peptide of 9 amino acids preferably has the following motif: a first conserved residue at the second position from the N-terminus selected from the group consisting of I, V, A and T and a second conserved residue at the C-terminal position selected from the group consisting of V, L, I, A and M. An alternate motif is one in which the first conserved residue at the second position from the N-terminus selected is from the group consisting of L, M, I, V, A and T and the second conserved residue at the C-terminal position selected from the group consisting of A and M. The amino acid at position 1 is preferably not an amino acid selected from the group consisting of D, and P. The amino acid at position 3 from the N-terminus is not an amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position 6 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K, H, D and E.

The HLA-A2.1 binding motif for peptide of 10 residues is as follows: a first conserved residue at the second position from the N-terminus selected from the group consisting of L, M, I, V, A, and T, and a second conserved residue at the C-terminal position selected from the group consisting of V, I, L, A and M. The first and second conserved residues are separated by 7 residues. Preferably, the amino acid at position 1 is not an amino acid selected from the group consisting of D, E and P. The N-terminal residue is not an amino acid selected from the group consisting of D and E. The residue at position 4 from the N-terminus is not an amino acid selected from the group consisting of A, K, R and H. The amino acid at position 5 from the N-terminus is not P. The amino acid at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at position 8 from the N-terminus is not amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position

9 from the N-terminus is not an amino acid selected from the group consisting of R, K and H.

5 The motif for HLA-A3.2 comprises from the N-terminus to C-terminus a first conserved residue of L, M, I, V, S, A, T and F at position 2 and a second conserved residue of K, R or Y at the C-terminal end. Other first conserved residues are C, G or D and alternatively E. Other second conserved residues are H or F. The first and second conserved residues are preferably separated by 6 to 7 residues.

10 The motif for HLA-A1 comprises from the N-terminus to the C-terminus a first conserved residue of T, S or M, a second conserved residue of D or E, and a third conserved residue of Y. Other second conserved residues are A, S or T. The first and second conserved residues are adjacent and are preferably separated from the third conserved residue by 6 to 7 residues. A second motif consists of a first conserved residue of E or D and a second conserved residue of Y where the first and second conserved residues are separated by 5 to 6 residues.

15 The motif for HLA-A11 comprises from the N-terminus to the C-terminus a first conserved residue of T, V, M, L, I, S, A, G, N, C D, or F at position 2 and a C-terminal conserved residue of K, R, Y or H. The first and second conserved residues are preferably separated by 6 or 7 residues.

20 The motif for HLA-A24.1 comprises from the N-terminus to the C-terminus a first conserved residue of Y, F or W at position 2 and a C terminal conserved residue of F, I, W, M or L. The first and second conserved residues are preferably separated by 6 to 7 residues.

25 These motifs are then used to define T cell epitopes from any desired antigen, particularly those associated with human viral diseases, cancers or autoimmune diseases, for which the amino acid sequence of the potential antigen or autoantigen targets is known.

30 Epitopes on a number of potential target proteins can be identified in this manner. Examples of suitable antigens include prostate specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, melanoma antigens (e.g., MAGE-1), human immunodeficiency virus (HIV) antigens, human papilloma virus (HPV) antigens, Lassa virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu.

Peptides comprising the epitopes from these antigens are synthesized and then tested for their ability to bind to the appropriate MHC molecules in assays using, for example, purified class I molecules and radioiodinated peptides and/or cells expressing empty class I molecules by, for instance, immunofluorescent staining and flow microfluorometry, peptide-dependent class I assembly assays, and inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary in vitro or in vivo CTL responses that can give rise to CTL populations capable of reacting with virally infected target cells or tumor cells as potential therapeutic agents.

The MHC class I antigens are encoded by the HLA-A, B, and C loci. HLA-A and B antigens are expressed at the cell surface at approximately equal densities, whereas the expression of HLA-C is significantly lower (perhaps as much as 10-fold lower). Each of these loci have a number of alleles. The peptide binding motifs of the invention are relatively specific for each allelic subtype.

For peptide-based vaccines, the peptides of the present invention preferably comprise a motif recognized by an MHC I molecule having a wide distribution in the human population. Since the MHC alleles occur at different frequencies within different ethnic groups and races, the choice of target MHC allele may depend upon the target population. Table 1 shows the frequency of various alleles at the HLA-A locus products among different races. For instance, the majority of the Caucasoid population can be covered by peptides which bind to four HLA-A allele subtypes, specifically HLA-A2.1, A1, A3.2, and A24.1. Similarly, the majority of the Asian population is encompassed with the addition of peptides binding to a fifth allele HLA-A11.2.

TABLE 1

<u>A Allele/Subtype</u>	<u>N(69)</u>	<u>A(54)</u>	<u>C(502)</u>
5	A1	10.1(7)	1.8(1)
	A2.1	11.5(8)	37.0(20)
	A2.2	10.1(7)	0
	A2.3	1.4(1)	5.5(3)
	A2.4	-	-
	A2.5	-	-
10	A3.1	1.4(1)	0
	A3.2	5.7(4)	5.5(3)
	A11.1	0	5.5(3)
	A11.2	5.7(4)	31.4(17)
	A11.3	0	3.7(2)
	A23	4.3(3)	-
15	A24	2.9(2)	27.7(15)
	A24.2	-	-
	A24.3	-	-
	A25	1.4(1)	-
	A26.1	4.3(3)	9.2(5)
	A26.2	7.2(5)	-
20	A26V	-	3.7(2)
	A28.1	10.1(7)	-
	A28.2	1.4(1)	-
	A29.1	1.4(1)	-
	A29.2	10.1(7)	1.8(1)
	A30.1	8.6(6)	-
25	A30.2	1.4(1)	-
	A30.3	7.2(5)	-
	A31	4.3(3)	7.4(4)
	A32	2.8(2)	-
	Aw33.1	8.6(6)	-
	Aw33.2	2.8(2)	16.6(9)
30	Aw34.1	1.4(1)	-
	Aw34.2	14.5(10)	-
	Aw36	5.9(4)	-

Table compiled from B. DuPont, Immunobiology of HLA, Vol. I, Histocompatibility Testing 1987, Springer-Verlag, New York 1989.

* N - negroid; A = Asian; C = caucasoid. Numbers in parenthesis represent the number of individuals included in the analysis.

40 The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus)

and the carboxyl group to the right (the C-terminus) of each amino acid residue. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

The procedures used to identify peptides of the present invention generally follow the methods disclosed in Falk et al., *Nature* 351:290 (1991), which is incorporated herein by reference. Briefly, the methods involve large-scale isolation of MHC class I molecules, typically by immunoprecipitation or affinity chromatography, from the appropriate cell or cell line. Examples of other methods for isolation of the desired MHC molecule equally well known to the artisan include ion exchange chromatography, lectin chromatography, size exclusion, high performance ligand chromatography, and a combination of all of the above techniques.

In the typical case, immunoprecipitation is used to isolate the desired allele. A number of protocols can be used, depending upon the specificity of the antibodies used. For example, allele-specific mAb reagents can be used for the affinity purification of the HLA-A, HLA-B, and HLA-C molecules. Several mAb reagents for the isolation of HLA-A molecules are available. The monoclonal BB7.2 is suitable for isolating HLA-A2 molecules. Affinity columns prepared with these mAbs using standard techniques are successfully used to purify the respective HLA-A allele products.

In addition to allele-specific mAbs, broadly reactive anti-HLA-A, B, C mAbs, such as W6/32 and B9.12.1, and one anti-HLA-B, C mAb, B1.23.2, could be used in alternative affinity purification protocols as described in previous applications.

The peptides bound to the peptide binding groove of the isolated MHC molecules are eluted typically using acid treatment. Peptides can also be dissociated from class I molecules by a variety of standard denaturing means, such as heat, pH, detergents, salts, chaotropic agents, or a combination thereof.

Peptide fractions are further separated from the MHC molecules by reversed-phase high performance liquid chromatography (HPLC) and sequenced. Peptides can be separated by a variety of other standard means well known to the artisan, including filtration, ultrafiltration, electrophoresis, size chromatography, precipitation with specific antibodies, ion exchange chromatography, isoelectrofocusing, and the like.

Sequencing of the isolated peptides can be performed according to standard techniques such as Edman degradation (Hunkapiller, M.W., et al., Methods Enzymol. 21, 399 [1983]). Other methods suitable for sequencing include mass spectrometry sequencing of individual peptides as previously described (Hunt, et al., Science 225:1261 (1992), which is incorporated herein by reference). Amino acid sequencing of bulk heterogenous peptides (e.g., pooled HPLC fractions) from different class I molecules typically reveals a characteristic sequence motif for each class I allele.

Definition of motifs specific for different class I alleles allows the identification of potential peptide epitopes from an antigenic protein whose amino acid sequence is known. Typically, identification of potential peptide epitopes is initially carried out using a computer to scan the amino acid sequence of a desired antigen for the presence of motifs. The epitopic sequences are then synthesized. The capacity to bind MHC Class molecules is measured in a variety of different ways. One means is a Class I molecule binding assay as described in the related applications, noted above. Other alternatives described in the literature include inhibition of antigen presentation (Sette, et al., J. Immunol. 141:3893 (1991), in vitro assembly assays (Townsend, et al., Cell 62:285 (1990), and FACS based assays using mutated cells, such as RMA-S (Mielke, et al., Eur. J. Immunol. 21:2963 (1991)).

Next, peptides that test positive in the MHC class I binding assay are assayed for the ability of the peptides to induce specific CTL responses in vitro. For instance, Antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells (Inaba, et al., J. Exp. Med. 166:182 (1987); Boog, Eur. J. Immunol. 18:219 [1988]).

Alternatively, mutant mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides, such as the mouse cell lines RMA-S (Kärre, et al., Nature, 319:675 (1986); Ljunggren, et al., Eur. J. Immunol.

21:2963-2970 (1991)), and the human somatic T cell hybrid, T-2 (Cerundolo, et al., Nature 345:449-452 (1990)) and which have been transfected with the appropriate human class I genes are conveniently used, when peptide is added to them, to test for the capacity of the peptide to induce *in vitro* primary CTL responses. Other eukaryotic cell lines which could be used include various insect cell lines such as mosquito larvae (ATCC cell lines CCL 125, 126, 1660, 1591, 6585, 6586), silkworm (ATTC CRL 8851), armyworm (ATCC CRL 1711), moth (ATCC CCL 80) and Drosophila cell lines such as a Schneider cell line (see Schneider J. Embryol. Exp. Morphol. 27:353-365 [1927]).

Peripheral blood lymphocytes are conveniently isolated following simple venipuncture or leukapheresis of normal donors or patients and used as the responder cell sources of CTL precursors. In one embodiment, the appropriate antigen-presenting cells are incubated with 10-100 μ M of peptide in serum-free media for 4 hours under appropriate culture conditions. The peptide-loaded antigen-presenting cells are then incubated with the responder cell populations *in vitro* for 7 to 10 days under optimized culture conditions. Positive CTL activation can be determined by assaying the cultures for the presence of CTLs that kill radiolabeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed form of the relevant virus or tumor antigen from which the peptide sequence was derived.

Specificity and MHC restriction of the CTL is determined by testing against different peptide target cells expressing appropriate or inappropriate human MHC class I. The peptides that test positive in the MHC binding assays and give rise to specific CTL responses are referred to herein as immunogenic peptides.

The immunogenic peptides can be prepared synthetically, or by recombinant DNA technology or from natural sources such as whole viruses or tumors. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides can be synthetically conjugated to native fragments or particles.

The polypeptides or peptides can be a variety of lengths, either in their neutral (uncharged) forms or in forms which are salts, and either free of modifications such as glycosylation, side chain oxidation, or phosphorylation or containing these modifications, subject to the condition that the modification not destroy the biological activity of the polypeptides as herein described.

Desirably, the peptide will be as small as possible while still maintaining substantially all of the biological activity of the large peptide. When possible, it may be desirable to optimize peptides of the invention to a length of 9 or 10 amino acid residues, commensurate in size with endogenously processed viral peptides or tumor cell peptides that are bound to MHC class I molecules on the cell surface.

Peptides having the desired activity may be modified as necessary to provide certain desired attributes, e.g., improved pharmacological characteristics, while increasing or at least retaining substantially all of the biological activity of the unmodified peptide to bind the desired MHC molecule and activate the appropriate T cell. For instance, the peptides may be subject to various changes, such as substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use, such as improved MHC binding. By conservative substitutions is meant replacing an amino acid residue with another which is biologically and/or chemically similar, e.g., one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala; Val, Ile, Leu, Met; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. The effect of single amino acid substitutions may also be probed using D-amino acids. Such modifications may be made using well known peptide synthesis procedures, as described in e.g., Merrifield, Science 232:341-347 (1986), Barany and Merrifield, The Peptides, Gross and Meienhofer, eds. (N.Y., Academic Press), pp. 1-284 (1979); and Stewart and Young, Solid Phase Peptide Synthesis, (Rockford, Ill., Pierce), 2d Ed. (1984), incorporated by reference herein.

The peptides can also be modified by extending or decreasing the compound's amino acid sequence, e.g., by the addition or deletion of amino acids. The peptides or analogs of the invention can also be modified by altering the order or composition of certain residues, it being readily appreciated that certain amino acid residues essential for biological activity, e.g., those at critical contact sites or conserved residues, may generally not be altered without an adverse effect on biological activity. The non-critical amino acids need not be limited to those naturally occurring in proteins, such as L- α -amino acids, or their D-isomers, but may include non-natural amino acids as well, such as β - γ - δ -amino acids, as well as many derivatives of L- α -amino acids.

Typically, a series of peptides with single amino acid substitutions are employed to determine the effect of electrostatic charge, hydrophobicity, etc. on binding.

For instance, a series of positively charged (e.g., Lys or Arg) or negatively charged (e.g., Glu) amino acid substitutions are made along the length of the peptide revealing different patterns of sensitivity towards various MHC molecules and T cell receptors. In addition, multiple substitutions using small, relatively neutral moieties such as Ala, Gly, Pro, or similar residues may be employed. The substitutions may be homo-oligomers or hetero-oligomers. The number and types of residues which are substituted or added depend on the spacing necessary between essential contact points and certain functional attributes which are sought (e.g., hydrophobicity versus hydrophilicity). Increased binding affinity for an MHC molecule or T cell receptor may also be achieved by such substitutions, compared to the affinity of the parent peptide. In any event, such substitutions should employ amino acid residues or other molecular fragments chosen to avoid, for example, steric and charge interference which might disrupt binding.

Amino acid substitutions are typically of single residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a final peptide. Substitutional variants are those in which at least one residue of a peptide has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the following Table 2 when it is desired to finely modulate the characteristics of the peptide.

TABLE 2

<u>Original Residue</u>	<u>Exemplary Substitution</u>
Ala	Ser
Arg	Lys, His
Asn	Gln
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Lys; Arg
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; His
Met	Leu; Ile
Phe	Tyr; Trp
Ser	Thr
Thr	Ser
Trp	Tyr; Phe
Tyr	Trp; Phe
Val	Ile; Leu
Pro	Gly

Substantial changes in function (e.g., affinity for MHC molecules or T cell receptors) are made by selecting substitutions that are less conservative than those in Table 2, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in peptide properties will be those in which (a) hydrophilic residue, e.g. seryl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a residue having an electropositive side chain, e.g., lysyl, 5 arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (c) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

The peptides may also comprise isosteres of two or more residues in the immunogenic peptide. An isostere as defined here is a sequence of two or more residues 10 that can be substituted for a second sequence because the steric conformation of the first sequence fits a binding site specific for the second sequence. The term specifically includes peptide backbone modifications well known to those skilled in the art. Such modifications include modifications of the amide nitrogen, the α -carbon, amide carbonyl, complete replacement of the amide bond, extensions, deletions or backbone crosslinks.

15 See, generally, Spatola, Chemistry and Biochemistry of Amino Acids, peptides and Proteins, Vol. VII (Weinstein ed., 1983).

Modifications of peptides with various amino acid mimetics or unnatural amino acids are particularly useful in increasing the stability of the peptide *in vivo*. Stability can be assayed in a number of ways. For instance, peptidases and various 20 biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef et al., Eur. J. Drug Metab. Pharmacokin. 11:291-302 (1986). Half life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows. Pooled human serum (Type AB, 25 non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI tissue culture media and used to test peptide stability. At 30 predetermined time intervals a small amount of reaction solution is removed and added to either 6% aqueous trichloracetic acid or ethanol. The cloudy reaction sample is cooled

(4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

The peptides of the present invention or analogs thereof which have CTL stimulating activity may be modified to provide desired attributes other than improved serum half life. For instance, the ability of the peptides to induce CTL activity can be enhanced by linkage to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Particularly preferred immunogenic peptides/T helper conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, e.g., Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the CTL peptide may be linked to the T helper peptide without a spacer.

The immunogenic peptide may be linked to the T helper peptide either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated. Exemplary T helper peptides include tetanus toxoid 830-843, influenza 307-319, malaria circumsporozoite 382-398 and 378-389.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes CTL. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the alpha and epsilon amino groups of a Lys residue and then linked, e.g., via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be injected directly in a micellar form, incorporated into a liposome or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment a particularly effective immunogen comprises palmitic acid attached to alpha and epsilon amino groups

of Lys, which is attached via linkage, e.g., Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, E. coli lipoproteins, such as tripalmitoyl-S-glycerylcysteinylseryl-serine (P₃CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide. See, Deres et al., 5 Nature 342:561-564 (1989), incorporated herein by reference. Peptides of the invention can be coupled to P₃CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Further, as the induction of neutralizing antibodies can also be primed with P₃CSS conjugated to a peptide which 10 displays an appropriate epitope, the two compositions can be combined to more effectively elicit both humoral and cell-mediated responses to infection.

In addition, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support, or 15 larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide. Modification at the C terminus in some cases may alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, e.g., by alkanoyl 20 (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, e.g., ammonia, methylamine, etc. In some instances these modifications may provide sites for linking to a support or other molecule.

The peptides of the invention can be prepared in a wide variety of ways. 25 Because of their relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, Solid Phase Peptide Synthesis, 2d. ed., Pierce Chemical Co. (1984), supra.

Alternatively, recombinant DNA technology may be employed wherein a 30 nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art,

as described generally in Sambrook et al., Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, New York (1982), which is incorporated herein by reference. Thus, fusion proteins which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

5 As the coding sequence for peptides of the length contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., J. Am. Chem. Soc. 103:3185 (1981), modification can be made simply by substituting the appropriate base(s) for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression 10 vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired 15 cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

20 The peptides of the present invention and pharmaceutical and vaccine compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent viral infection and cancer. Examples of diseases which can be treated using the immunogenic peptides of the invention include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV and 25 condyloma acuminatum.

For pharmaceutical compositions, the immunogenic peptides of the invention are administered to an individual already suffering from cancer or infected with the virus of interest. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as 30 appropriate. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the virus or tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to

accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial 5 immunization (that is for therapeutic or prophylactic administration) from about 1.0 μ g to about 5000 μ g of peptide for a 70 kg patient, followed by boosting dosages of from about 1.0 μ g to about 1000 μ g of peptide pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring specific CTL activity in the patient's blood. It must be kept in mind that the peptides and compositions of the 10 present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions.

15 For therapeutic use, administration should begin at the first sign of viral infection or the detection or surgical removal of tumors or shortly after diagnosis in the case of acute infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In chronic infection, loading doses followed by boosting doses may be required.

20 Treatment of an infected individual with the compositions of the invention may hasten resolution of the infection in acutely infected individuals. For those individuals susceptible (or predisposed) to developing chronic infection the compositions are particularly useful in methods for preventing the evolution from acute to chronic infection. Where the susceptible individuals are identified prior to or during infection, for instance, 25 as described herein, the composition can be targeted to them, minimizing need for administration to a larger population.

The peptide compositions can also be used for the treatment of chronic infection and to stimulate the immune system to eliminate virus-infected cells in carriers. It is important to provide an amount of immuno-potentiating peptide in a formulation and 30 mode of administration sufficient to effectively stimulate a cytotoxic T cell response. Thus, for treatment of chronic infection, a representative dose is in the range of about 1.0 μ g to about 5000 μ g, preferably about 5 μ g to 1000 μ g for a 70 kg patient per dose.

5 Immunizing doses followed by boosting doses at established intervals, e.g., from one to four weeks, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been

eliminated or substantially abated and for a period thereafter.

10 The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be

15 packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride,

20 calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

25 The concentration of CTL stimulatory peptides of the invention in the pharmaceutical formulations can vary widely, i.e., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected.

30 The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or targeted selectively to infected cells, as well as increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to, e.g., a receptor prevalent among lymphoid cells, such as monoclonal

antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the selected therapeutic/immunogenic peptide compositions. Liposomes for use in the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al., Ann. Rev. Biophys. Bioeng. 10:467 (1980), U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, incorporated herein by reference.

For targeting to the immune cells, a ligand to be incorporated into the liposome can include, e.g., antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight

of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, e.g., lecithin for intranasal delivery.

In another aspect the present invention is directed to vaccines which contain as an active ingredient an immunogenically effective amount of an immunogenic peptide as described herein. The peptide(s) may be introduced into a host, including humans, linked to its own carrier or as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the virus or tumor cells.

Useful carriers are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B virus recombinant vaccine and the like. The vaccines can also contain a physiologically tolerable (acceptable) diluent such as water, phosphate buffered saline, or saline, and further typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art. And, as mentioned above, CTL responses can be primed by conjugating peptides of the invention to lipids, such as P₃CSS. Upon immunization with a peptide composition as described herein, via injection, aerosol, oral, transdermal or other route, the immune system of the host responds to the vaccine by producing large amounts of CTLs specific for the desired antigen, and the host becomes at least partially immune to later infection, or resistant to developing chronic infection.

Vaccine compositions containing the peptides of the invention are administered to a patient susceptible to or otherwise at risk of viral infection or cancer to elicit an immune response against the antigen and thus enhance the patient's own immune response capabilities. Such an amount is defined to be an "immunogenically effective dose." In this use, the precise amounts again depend on the patient's state of health and weight, the mode of administration, the nature of the formulation, etc., but generally range from about 1.0 μ g to about 5000 μ g per 70 kilogram patient, more commonly from about 10 μ g to about 500 μ g mg per 70 kg of body weight.

In some instances it may be desirable to combine the peptide vaccines of the invention with vaccines which induce neutralizing antibody responses to the virus of interest, particularly to viral envelope antigens.

For therapeutic or immunization purposes, nucleic acids encoding one or more of the peptides of the invention can also be administered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nucleic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff *et. al.*, *Science* 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. The nucleic acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO 96/18372; WO 93/24640; Mannino and Gould-Fogerite (1988) *BioTechniques* 6(7): 682-691; Rose U.S. Pat No. 5,279,833; WO 91/06309; and Felgner *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 7413-7414. The peptides of the invention can also be expressed by attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848, incorporated herein by reference. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.* (*Nature* 351:456-460 (1991)) which is incorporated herein by reference. A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g., *Salmonella typhi* vectors and the like, will be apparent to those skilled in the art from the description herein.

A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding multiple epitopes of the invention. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding

DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL epitopes.

The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are included in the vector to ensure expression in the target cells. Several vector elements are required: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human cytomegalovirus (hCMV) promoter. See, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences can also be considered for increasing minigene expression. It has recently been proposed that immunostimulatory sequences (ISSs or CpGs) play a role in the immunogenicity of DNA vaccines. These sequences could be included in the vector, outside the minigene coding sequence, if found to enhance immunogenicity.

In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially

enhance the immune response if co-expressed include cytokines (e.g., IL2, IL12, GM-CSF), cytokine-inducing molecules (e.g. LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

Therapeutic quantities of plasmid DNA are produced by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate fermentation medium (such as Terrific Broth), and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by Quiagen. If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques may become available. As noted above, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and MHC class I presentation of minigene-encoded CTL epitopes. The plasmid DNA is

introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be 5 co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 labeled and used as target cells for epitope-specific CTL lines. Cytolysis, detected by 51Cr release, indicates production of MHC presentation of minigene-encoded CTL epitopes.

10 *In vivo* immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human MHC molecules are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g. IM for DNA in PBS, IP for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for 1 week in the presence of peptides encoding each epitope being tested. These effector cells (CTLs) are assayed 15 for cytolysis of peptide-loaded, chromium-51 labeled target cells using standard techniques. Lysis of target cells sensitized by MHC loading of peptides corresponding to minigene-encoded epitopes demonstrates DNA vaccine function for *in vivo* induction of CTLs.

20 Antigenic peptides may be used to elicit CTL *ex vivo*, as well. The resulting CTL, can be used to treat chronic infections (viral or bacterial) or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a peptide vaccine approach of therapy. *Ex vivo* CTL responses to a particular pathogen (infectious agent or tumor antigen) are induced by incubating in tissue culture the patient's CTL precursor cells (CTLp) together with a source of antigen-presenting cells (APC) and the 25 appropriate immunogenic peptide. After an appropriate incubation time (typically 1-4 weeks), in which the CTLp are activated and mature and expand into effector CTL, the cells are infused back into the patient, where they will destroy their specific target cell (an infected cell or a tumor cell).

30 The peptides may also find use as diagnostic reagents. For example, a peptide of the invention may be used to determine the susceptibility of a particular individual to a treatment regimen which employs the peptide or related peptides, and thus may be helpful in modifying an existing treatment protocol or in determining a prognosis for an affected

individual. In addition, the peptides may also be used to predict which individuals will be at substantial risk for developing chronic infection.

The following example is offered by way of illustration, not by way of limitation.

5

Example 1

Class I antigen isolation was carried out as described in the related applications, noted above. Naturally processed peptides were then isolated and sequenced as described there. An allele-specific motif and algorithms were determined and quantitative binding assays were carried out.

10

Using the motifs identified above for various HLA alleles, amino acid sequences from a number of antigens were analyzed for the presence of these motifs. Tables 3- ** provide the results of these searches.

15

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

20

Table 3

25

30

Sequence	Antigen	Molecule
FTFSPTYKAFLSK	HBV	POL
GTLPQEHVVLKLK	HBV	POL
FTFSPTYKAPLCK	HBV	POL
GTLPQEHVVLKIK	HBV	POL
LVVSYVNTNMGLK	HBV	POL
STTDLEAYFKDCLFK	HBV	X
LVVSYVNVMGLK	HBV	NUC
GTLPQDHIVQKIK	HBV	POL
STSSCLHQSAVRK	HBV	POL
TTVNAHQILPKVLHK	HBV	X
RTPARVTGGVFLVDK	HBV	POL

Sequence	Antigen	Molecule
HTTNFASK	HBV ayw	
FTFSPTYK	HBV ayw	
PTYKAFLCKQY	HBVayw	
CTTPAQGTSMY	HBVayw	
PTSCPPTCPGY	HBVayw	
FSQFSRGNY	HBVayw	
LMPLYACIQSK	HBVayw	
RVTGGVFLVDK	HBVayw	POL
HTLWKAGILYK	HBVayw	
QTRHYLHTLWK	HBVayw	
GTDNSVVLRSK	HBVayw	
SYVNTNMGLKF	HBVayw	
LYSILSPF	HBVayw	
WYWGPSLYSIL	HBVayw	
LYSILSPFLPL	HBVayw	
PYKEFGATVEL	HBVayw	
CTWMNSTGFTK	HCV	
MYVGDLCGSVF	HCV	
VYLLPRRGPRL	HCV	
ITKIQNF瑞VYY	HIV	
KVYLAWVPAHK	HIV	
KMIGGIGGF瑞K	HIV	
IVASCDKCQLK	HIV	
KVKQWPLTEEK	HIV	
TVNDIQKLVGK	HIV	
DVKQLTEAVQK	HIV	
AVVIQDNSDIK	HIV	
WTYQIYQEPPFK	HIV	
VTVYYGVPVWK	HIV	
LTEDRWNKPQK	HIV	
ATDIQTKELQK	HIV	
OTKELOKOITK	HIV	

Sequence	Antigen	Molecule
WTVQPIVLPEK	HIV	
QVPLRPMTYK	HIV nef 73-82	
QVPLYPMTFK	HIV nef 73-82	
VPLRPMTYK	HIV nef 74-82	
AVDLYHFLK	HIV nef 84-94	
AVDLSHFLK	HIV nef 84-94	
ATLYCVHQR	HIV, p17, 82-90	
RLRDLLLIV	HIV-1 NL43 768-776	
RLRDLLLIVTR	HIV-1 NL43 768-778	
RLRDYLLIVTR	HIV-1 NL43 768-778	
LRDLLLIVTR	HIV-1 NL43 769-778	
QIYQEPFKNLK	HIV-1 RT 507-517	
AVFIHNFK	HIVcon	
RTLNAWVK	HIVcon	
ETAYF1LK	HIVcon	
RLRPGGKKK	HIVgag p17/2	
KIRLRPGGKK	HIVgag p17/2	
KIRLRPGGK	HIVgag p17/2	
ETTDLYCY	HPV16	E7
GTLGIVCPICSQK	HPV16	E7

Sequence	Antigen	Molecule
LMGTLGIVCPICSQK	HPV16	E7
AVCDKCLK	HPV16	E6
PYAVCDKCLKF	HPV16	E6
HYCYSLYGTTL	HPV16	E6
FYSRIREL	HPV16	E6
TLEKLTNTGLY	HPV18	E6
KTVLELTEVFEFAFK	HPV18	E6
TMLCMCCK	HPV18	E7
NTSLQDIEITCVYCK	HPV18	E6
EVFEFAFK	HPV18	E6
KQSSKALQR	Leukemia-	β3A2 CMI
ATGFKQSSK	Leukemia	β3A2 CMI
HSATGFKQSSK	Leukemia	β3A2 CMI
FKQSSKALQR	Leukemia	β3A2 CMI
VTCLGLSY	MAGE1	
ITKKVADLVGFLLLK	MAGE1	
LVGFLLLK	MAGE1	
VTKAEMLESVIKNYK	MAGE1	
TSCILESFLFR	MAGE1	
NYKHCPPEI	MAGE1	
SYVLVTCL	MAGE1	
ETDPISHTY	MAGE1 (a)	
ETDPTSHLY	MAGE1 (a)	
ETDPTSNTY	MAGE1 (a)	
ETDPTSHVY	MAGE1 (a)	
ETDPTSHSY	MAGE1 (a)	
ETDPASHTY	MAGE1 (a)	
EVDPSTSHTY	MAGE1 (a)	
ETDPTGHTY	MAGE1 (a)	
ETDRTSHTY	MAGE1 (a)	
EADPTSHTY	MAGE1 (a)	
ETVPTSHTY	MAGE1 (a)	

Sequence	Antigen	Molecule
ETDPTSHTY	MAGE1	
	consensus	
ETDPTGHSY	MAGE1 T(a)	
MFPDLESEF	MAGE2	
TTINYTLWR	MAGE2	
VIFSKASEY	MAGE2	
LVHFLLLKY	MAGE2	
LVHFLLLKY	MAGE2	
LVHFLLLKYR	MAGE2	
PVIFSKASEY	MAGE2	
STTINYTLWR	MAGE2	
VVEVVPISH	MAGE2	
EYLQLVFGI	MAGE2	
IFSKASEYL	MAGE2	
SFSTTINYTL	MAGE2	
LYILVTCIGL	MAGE2	
FATCLGLSY	MAGE3	
VVGNWQYFFPVIFSK	MAGE3	
LIIVLAIIR	MAGE3	
YFFPVIFSK	MAGE3	
NWQYFFPVVI	MAGE3	
NWQYFFPVIF	MAGE3	
IFSKASSSL	MAGE3	
EVDPTSNTY	MAGE41	
RYPLTFGWCY	nef/182	
RYPLTFGWC	nef/182	
ATOQIPSYK	PAP	
LTELTYFEK	PAP	
HSFPHPPLY	PSA	
TQEPALGTTCY	PSA	
VTKFMLCAGRWTGGK	PSA	
HVISNDVCAQVHPQK	PSA	

Sequence	Antigen	Molecule
LYDMSLLKNRF	PSA	
ETDPTGHSY	T2 analog of MAGE-3	

Table 4

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.030	IILDMLRILY	9	c-ERB2			42		9.1	0.037	0.002		
1.0346	LLDIDETEV	9	c-ERB2			869		7.6	0.033	0		
1.0305	GTOLEFDENY	9	c-ERB2			104		0.16	0	0.028		
1.0355	LTCSPOPEY	9	c-ERB2			1131		0.13	0	0.0061		
1.0317	ETLEENETY	9	c-ERB2			401		0.043	0.0002	0.0002		
1.0339	QLVITQLMPY	9	c-ERB2			793		0.024	0.011	0.0039		
1.0349	PTIKGSDVWSY	10	c-ERB2			599		2.7	0.003	0.005		
1.0347	RLLDIDETEV	10	c-ERB2			868		1.3	0.017	0		
1.0313	TLEENETY	10	c-ERB2			402		1.1	0	0		
1.0337	YMMAGCIVGSPY	10	c-ERB2			772		1.1	0	0.010	0.012	0
1.0364	GTTTAENPEY	10	c-ERB2			1239		0.63	0.002	0.002		
1.0324	RVVQCLPPEY	10	c-ERB2			545		0.0015	0.035	0.0050		
1.0305	LQQRNPOLCY	10	c-ERB2			154		0.030	0.0012	0.0002		
1.0323	WVQGHNLLTY	10	c-ERB2			55		0.018	0.0024	0.011		
1.0356	MCDIVDABEV	10	c-ERB2			1014		0.012	0.0002	0.0002		
1.0328	KDRTYTMRE	9	c-ERB2			661		3.11	0.76	0.0018		
1.0327	WFGCILKR	9	c-ERB2			669		3.11	0.11	0.72		
1.0344	LVKSPNHRVK	9	c-ERB2			852		3.11	0.48	0.070		
1.0333	VLLRTNSPK	9	c-ERB2			754		3.11	0.40	0.013		
1.0329	ILKIKRROQK	9	c-ERB2			623		3.11	0.39	0.0077		
1.0311	ILWKDIFHK	9	c-ERB2			167		3.11	0.20	0.31		
1.0323	KIDDFGLAR	9	c-ERB2			860		3.11	0.17	0.24		
1.0369	GIVFGILK	9	c-ERB2			668		3.11	0.007	0.009		
1.0329	QVCTGDK	9	c-ERB2			24		3.11	0.007	0.032		
1.0321	LLDHYREN	9	c-ERB2			806		3.11	0.037	0.0006		
1.0326	CVNCOSFLR	9	c-ERB2			528		3.11	0.0013	0.01		
1.0323	TYCAGGCCAR	9	c-ERB2			218		3.11	0.004	0.023		
1.0331	ILKETELSK	9	c-ERB2			711		3.11	0.019	0.0023		
1.0324	VTAEDGTO	9	c-ERB2			322		3.11	0.0002	0.014		
1.0326	DLSTMFWK	9	c-ERB2			607		3.11	0.0005	0.010		
1.0312	RLVHRDLAAR	10	c-ERB2			166		3.11	0.043	3.6		
1.0321	UNWCMQIAK	10	c-ERB2			327		3.11	0.021	0.61		
1.0323	NDVYMMVAK	10	c-ERB2			751		3.11	0.38	0.22		
						141		3.11	0.20	0.013		
						840		3.11	0.18	0		
						948		3.11	0.14	0.14		
						948		3.11	0.013	0.12		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0731	RILKETELRK	10	c-ERB2			713	3.11		0.057	0.11		
1.0745	VLVLSPIPNIVK	10	c-ERB2			851	3.11		0.062	0.072		
1.1131	SVRQNLQVIR	10	c-ERB2			423	3.11		0.017	0.075		
1.1133	IITVVPWDQFLR	10	c-ERB2			478	3.11		0.0035	0.072		
1.1127	ILKCCGVLIQR	10	c-ERB2			14H	3.11		0.040	0.0055		
1.1143	LVSEPSRMR	10	c-ERB2			972	3.11		0.0072	0.033		
1.1136	GVVFCILIKR	10	c-ERB2			668	3.11		0.018	0.033		
1.0726	CVARCPSCVK	10	c-ERB2			596	3.11		0.022	0.0047		
1.1137	WVFCILIKR	10	c-ERB2			669	3.11		0.0030	0.016		
1.0728	GILIKRRQQK	10	c-ERB2			672	3.11		0.015	0.0014		
1.1129	RTV/CAGCCAR	10	c-ERB2			217	3.11		0.0068	0.013		
1.1134	GLAHCIIQCAR	10	c-ERB2			508	3.11		0.011	0		
1.1139	KIPVAIKVLR	10	c-ERB2			747	3.11		0.0009	0.0099		

Pepptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0291	VCEDADYFEEY	9	EBNA1			409	1	0.016				
1.0295	PLRESIVCY	9	EBNA1			553	1	0.010				
1.0681	PGCEADYFEEY	10	EBNA1			408	1	0.015				
1.0683	GTWVAGCIVRY	10	EBNA1			501	1	0.014				
1.0293	GVFVYGGSK	9	EBNA1			506	3,11		0.30	0.61		
1.1016	KTSLYNLRR	9	EBNA1			514	3,11		0.31	0.12		
1.0297	AIKDLVMTK	9	EBNA1			578	3,11		0.048	0.034		
1.0687	QTHIFAEVLUK	10	EBNA1			567	3,11		0.010	0.21		
1.1124	GTALAIQOCR	10	EBNA1			523	3,11		0.0028	0.056		

Pepptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
5.005	CTEIKLSDY	9	FLU	A	NP	44	1	36				
5.006	STIELRSRY	9	FLU	A	NP	377	1	0.020				
5.004	ILRCGVAK	9	FLU	A	NP	265	3		1.5	0.0037		
5.001	RMCHNLKCK	9	FLU	A	NP	221	3		0.27	0.002		
5.006	LMQGSTLPR	9	FLU	A	NP	165	3		0.031	0.10		
5.008	MIDGIGRPF	9	FLU	A	NP	32	3		0.059	0.0010		
5.009	MVLSAFDER	9	FLU	A	NP	66	3		0.0016	0.041		
5.004	YIQMCTELK	9	FLU	A	NP	40	3		0.0031	0.030		
5.002	GINDRNFWR	9	FLU	A	NP	200	3		0.0028	0.024		
5.0104	SLMQCSTLPR	10	FLU	A	NP	165	3		0.12	0.84		
5.005	KMIDGIGRPF	10	FLU	A	NP	31	3		0.50	0.0079		
5.006	LILAGSVAHK	10	FLU	A	NP	264	3		0.36	0.037		
5.0102	ESCAAGAAVK	10	FLU	A	NP	175	3		0.019	0.0046		
5.0105	STTEILRSRY	10	FLU	A	NP	376	3		0.0018	0.016		
5.0103	RSRYWAAKTR	10	FLU	A	NP	382	3		0.012	0		
5.0101	RAVLSDAFDER	10	FLU	A	NP	65	3		0.0014	0.010		
5.0061	PTIQMCTEL	9	FLU	A	NP	39	24			2.9		
5.0060	AYVEMKQIL	9	FLU	A	NP	218	24			0.031		
5.0112	RFYQMCTEL	10	FLU	A	NP	38	24			0.15		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A21	A32	A11	A24
1.0155	LLDTASALY	9	HBV	adr	CORE	420	1	25	0.0007	0		
1.0166	SLDVSAAFY	9	HBV	adr	POL	1001	1	172	0.0007	0.0006		
2.0123	PTTCRTSLY	9	HBV	ALL		1,382	1	13	0.0008	0		
2.0126	MSTTDILEAY	9	HBV	adr		1,521	1	0.85	<0.0006	0		
1.0208	PTTCRTSLY	9	HBV	adr	POL	1382	1	0.77	0	0		
1.0387	LTKQYQNLHY	9	HBV	adr	POL	1260	1	0.90	0.0003	0.0005		
1.0166	KVCNFTGFLY	9	HBV	adr	POL	629	1	0.68	0.30	0.014		
2.0127	MSTTDILEAY	9	HBV	adr	POL	1,550	1	0.67				
2.0120	FSQFERNQY	9	HBV	87W		984	1	0.67				
2.0112	PSWIVAFAY	9	HBV	adr		316	1	0.64				
2.0119	QSAVKREAY	9	HBV	adr		881	1	0.25				
1.0174	PLDKGKPY	9	HBV	adr	POL	698	1	0.19	<0.0002	<0.0002		
1.0278	SLMLVITY	9	HBV	adr	POL	1082	1	0.17				
2.0115	ASRDIVLY	9	HBV	87W		499	1	0.03				
2.0124	PSRCRGLY	9	HBV	adr/adr		1,364	1	0.011				
2.0211	SSTSERINY	9	HBV	adr		1,036	1	0.0077				
1.0519	DLDTASALY	10	HBV	adr	CORE	419	1	11.1	0	0		
1.0513	LLDPVPRVGLY	10	HBV	adr	ENV	120	1	6.3	0.17	0		
2.0239	LSLIVSAAFY	10	HBV	ALL		1,000	1	4.2	<0.0009	0.0037		
1.0511	FLCQGQYHLY	10	HBV	adr	POL	1250	1	1.1	0.0023	0.014	0.0048	0.007
2.0216	QTRGRKHLHY	10	HBV	87W	POL	1087	1	1.1	0.0056	0.012		
2.0244	KTYGRKHLHY	10	HBV	adr		1,098	1	0.69	0.0003	0.59	0.22	0
1.0791	KTYGRKHLHY	10	HBV	adr	POL	108	1	0.57	0.0020	0.53	0.35	0.0001
2.0242	QTRGRKHLHY	10	HBV	87W	POL	1,087	1	0.37	0.0037	0.011		
1.0556	KTRGRKHLHY	10	HBV	adr	POL	1,089	1	0.34	0.0023	0.004	0.000	0
2.0241	KTRGRKHLHY	10	HBV	adr		1,089	1	0.30	0.0007	0.15	0.09	0
1.0766	LQDPVPRVLY	10	HBV	adr	ENV	120	1	0.21	0.014	0		
1.0806	TTPAQCTSMY	10	HBV	adr	ENV	288	1	0.20	0	0		
2.0240	LSSTSERINY	10	HBV	adr		1,035	1	0.20	<0.0009	0		
1.0541	PLDKGKPY	10	HBV	adr	POL	698	1	0.16	0	0		
2.0239	HSASRCSQPY	10	HBV	87W		767	1	0.15	0	0.019	0.017	0
1.0793	FLTRQYQMLY	10	HBV	adr	POL	1279	1	0.12	0	0		
2.0237	RSASRCSQPY	10	HBV	adr/adr		738	1	0.11	0	0.0133	0.020	0
1.0774	WLWCMDIDPY	10	HBV	adr	CORE	416	1	0.081	<0.0002	<0.0002		
2.0233	TPPAQCTSMY	10	HBV	87W		288	1	0.066				
1.0542	ITLWIKAGILY	10	HBV	adr	POL	723	1	0.030				
2.0231	TSCMPCPY	10	HBV	adr		226	1	0.018				

Pepptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0246	KSVQIILESLY	10	HBV	adw	POL	1,161	1	0.016				
1.0910	NLYVPSLLY	10	HBV	adw	POL	1059	1	0.015				
2.0089	LYQOTGRK	9	HBV	syw	POL	104	3		1.8	0.64		
2.0116	IMPARYPK	9	HBV	syw	POL	713	3		0.99	1.5		
2.0082	CLIQSPVVK	9	HBV	syw	POL	867	3		0.14	0.025		
5.0056	SAICSVVRR	9	HBV		POL	531	3		40.000	0.067		
2.0077	HLHQDIIKK	9	HBV	syw	POL	686	3		0.041	0.0075		
2.0219	SLPQEHHIQK	10	HBV	syw	POL	1197	3		0.35	4.2		
2.0224	SMIFPSCCTK	10	HBV	adw/adw		295	3		0.43	1.9		
2.0225	SMIFPSCCTK	10	HBV	syw		295	3		1.1	1.79		
5.0107	QAFITSPYK	10	HBV		POL	665	3		0.15	1.3		
2.0214	LLYQDNGK	10	HBV	syw	POL	1083	3		0.09	0.021		
2.0245	YMDDDVILGAK	10	HBV	ALL		1,123	3		0.16	0.076		
5.0108	TSACSVVRR	10	HBV		POL	530	3		0.0006	0.013		
2.0024	PTKARFLK	9	HBV	syw	POL	1263	11		0.020	0.005		
2.0064	PTDLRATK	9	HBV	adw		1552	11		0.0002	0.016		
2.0061	KYTSPPWLL	9	HBV	ALL		1,230	24			3.6		
2.0059	LYAATPML	9	HBV	adw		1,159	24			3.2		
2.0046	PTMUTTML	9	HBV	adw		669	24			2.1		
2.0045	LYSTVTPP	9	HBV	adw/syw		665	24			1.9		
2.0044	PTPKVTKL	9	HBV	syw		718	24			1.7		
2.0049	PTPKVTKL	9	HBV	adw		718	24			1.6		
2.0039	LYSILSPFL	9	HBV	syw		368	24			0.50		
2.0044	LYSTVTPV	9	HBV	adw		636	24			0.37		
2.0038	LYNIISSPFL	9	HBV	adw		368	24			0.34		
2.0051	NYRVSWYCF	9	HBV	syw		991	24			0.18		
2.0060	HYRQHML	9	HBV	adw/syw		743	24			0.15		
2.0047	HYFKTHML	9	HBV	adw		714	24			0.057		
2.0060	GYPALMPLY	9	HBV	ALL		1,224	24			0.049		
5.0062	AYRPPNAP	9	HBV		NUC:XNUCFUS	131	24			0.076		
2.0064	LYQTCRKL	9	HBV	syw		1,085	24			0.014		
2.0043	SYQHFRRL	9	HBV	syw		607	24			0.011		
2.0181	LYSHPILCF	10	HBV	ALL		1,077	24			1.1		
2.0182	LYAATVNFL	10	HBV	adw		1,149	24			0.32		
2.0180	LYRPLSLPF	10	HBV	adw		1,371	24			0.25		
2.0174	SYQHFRRL	10	HBV	syw		607	24			0.16		
2.0173	SYQHFRKL	10	HBV	adw/adw		578	24			0.066		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.076	YYPEELVNLHY	10	HBV	Pyw		735	24				0.040	
2.077	AYTRPNAPI	10	HBV	AlL		521	24				0.022	
2.071	GYRWMCLRRF	10	HBV	AlL		234	24				0.011	
5.015	NFLSLCHL	10	HBV		POL	572	24				0.099	
1.037	YVSLMLLYK	9	HBV	adw	POL	1060	3.11				0.31	7.4
1.038	LLYIKTFCRK	9	HBV	adw	POL	1066	3.11				5.0	0.30
1.039	LLYIKTYCRK	9	HBV	adw	POL	1095	3.11				2.5	0.40
1.070	VTKMLPLDK	9	HBV	adw	POL	722	3.11				0.014	1.3
1.076	RYVYLHLTLWK	9	HBV	adw	POL	719	3.11				1.2	0.010
1.037	STVPSFNPK	9	HBV	adw	POL	668	3.11				0.021	0.93
1.0215	TTDILEAVRK	9	HBV	adw	X	1523	3.11				0.006	0.92
1.0648	YVSLLLYK	9	HBV	adw	POL	1061	3.11				0.39	0.92
1.0383	PTTKARFLTK	9	HBV	adw	POL	1274	3.11				0.17	0.71
1.0987	HLTVPRARQ	9	HBV	adw	POL	1257	3.11				0.54	0.0080
1.0358	STNRQLGRK	9	HBV	adw	ENV	85	3.11				0.51	0.34
1.0991	ALRFTSARR	9	HBV	adw	X	1488	3.11				0.44	<0.0005
1.0197	PVNRPDWRK	9	HBV	adw	POL	1197	3.11				0.080	0.41
1.0364	TVNEDVRLK	9	HBV	adw	POL	703	3.11				0.016	0.40
1.1041	WVNHYRQTR	9	HBV	adw	POL	740	3.11				0.030	0.33
1.0132	STTSCTCK	9	HBV	adw	ENV	277	3.11				0.011	0.29
1.0213	QVPLKLHK	9	HBV	adw	X	1905	3.11				0.10	0.29
1.0172	LTKMLHDK	9	HBV	adw	POL	693	3.11				0.0089	0.23
1.0374	CLHQSAVHK	9	HBV	adw	POL	678	3.11				0.22	0.017
1.0960	WVDFSQFSR	9	HBV	adw	POL	963	3.11				0.011	0.20
1.0382	PLYACIQAK	9	HBV	adw	POL	1259	3.11				0.18	0.04
2.0274	YVNTNMGLK	9	HBV	adw	CORE	507	3.11				0.16	0.048
1.0199	PLYACIOSK	9	HBV	adw	POL	1220	3.11				0.11	0.018
1.0372	RLADEGLVR	9	HBV	adw	POL	601	3.11				0.10	0.025
1.0976	AVNHYFKTR	9	HBV	adw	POL	711	3.11				0.0071	0.098
1.0975	RLKLIMPAR	9	HBV	adw	POL	680	3.11				0.095	0.002
1.0377	ILYKRETRR	9	HBV	adw	POL	730	3.11				0.095	<0.005
1.0993	KVFVLLGCCR	9	HBV	adw	X	1548	3.11				0.042	0.082
1.0165	NVSIPWTHK	9	HBV	adw	POL	621	3.11				0.072	0.076
1.0982	LLYIKTFCR	9	HBV	adw	POL	1065	3.11				0.072	0.0045
1.0978	RLVQFQSTR	9	HBV	adw	POL	757	3.11				0.068	0.032
1.0219	FVLGGCCRHK	9	HBV	adw	X	1550	3.11				0.085	0.019
1.1042	RLVQFSTR	9	HBV	adw	POL	766	3.11				0.064	0.002

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.1043	MLLYKTYGR	9	HBV	adv	POL	1094	3.11	0.061	0.0032			
1.1070	TNEKRRRK	9	HBV	adv	POL	674	3.11	0.048	0.0037			
1.1045	NLYPVVARQR	9	HBV	adv	POL	1296	3.11	0.042	0.0011			
1.1046	LPRRPTCR	9	HBV	adv	POL	1407	3.11	0.021	0			
1.1085	LVSCGVWIR	9	HBV	adv	CORE	509	3.11	0.0033	0.0020			
1.1081	LVSCGGLPR	9	HBV	adv	POL	1022	3.11	0.0008	0.015			
1.1067	HISCLTCR	9	HBV	adv	CORE	494	3.11	0.013	0.011			
1.1047	SVPSRIFDR	9	HBV	adv	POL	1424	3.11	0.0007	0.010			
1.1089	SVPSHIDR	9	HBV	adv	POL	1395	3.11	0.0004	0.010			
1.1064	TLRQEHTVLK	10	HBV	adv	POL	1179	3.11	0.092	5.6			
2.1005	TVPVFNPHWK	10	HBV	sym	POL	669	3.11	0.0057	4.2			
1.1043	TLWKGAGILYK	10	HBV	adv	POL	724	3.11	3.5	1.0			
1.0807	SMYPSCCCTK	10	HBV	sym	ENV	295	3.11	1.5	3.4			
1.1153	RLPYRPTGR	10	HBV	adv	POL	1405	3.11	2.8	0.030			
1.0584	STTDLPLAVPK	10	HBV	adv	X	1522	3.11	0.0066	2.7			
1.0584	LLLYKTRGRK	10	HBV	adv	POL	1065	3.11	2.3	0.012			
1.0799	TVNAHARNLPK	10	HBV	adv	X	1529	3.11	0.02	0.65			
1.0886	RAYFKDQFLK	10	HBV	adv	X	1527	3.11	0.007	0.74			
1.1081	LVDVDPQPSK	10	HBV	adv	POL	962	3.11	0.0009	0.63			
1.0789	MLLYKTYGRK	10	HBV	adv	POL	1094	3.11	0.01	0.020			
1.0546	TAVSHLSTSK	10	HBV	adv	POL	858	3.11	0.26	0.092			
1.0562	SLGCHLHNPK	10	HBV	adv	POL	1150	3.11	0.20	0.078			
1.1152	RIGLYTRPLR	10	HBV	adv	POL	1397	3.11	0.19	0.0049			
1.0547	VTGCVFLYK	10	HBV	adv	POL	943	3.11	0.038	0.17			
1.1150	RIRTRPTPAR	10	HBV	adv	POL	962	3.11	0.17	0.002			
1.0591	TWNGHQVLPK	10	HBV	adv	X	1500	3.11	0.073	0.092			
1.1091	SUFPQPTCR	10	HBV	adv	POL	1377	3.11	0.077	0.043			
1.1072	TLPETTVVRR	10	HBV	adv	CORE	532	3.11	0.0003	0.075			
1.1089	GTDNNSVLSR	10	HBV	adv	POL	1320	3.11	0.025	0.072			
1.1071	STLPETTVR	10	HBV	adv	CORE	531	3.11	0.0005	0.068			
2.0210	KVTKYLPIDK	10	HBV	sym	POL	721	3.11	0.027	0.053			
1.1148	STRHGDKSR	10	HBV	adv	POL	792	3.11	0.0057	0.038			
1.0735	VLSCWVWLQFR	10	HBV	adv	POL	923	3.11	0.029	0.007			
1.0781	NVTKYLPIDK	10	HBV	adv	POL	721	3.11	0.0004	0.023			
1.1092	RVCQCLDPAR	10	HBV	adv	X	1422	3.11	0.019	0.012			
1.0793	SLCIIIILNPK	10	HBV	adv	POL	1179	3.11	0.017	0.014			
1.0899	YLVSFCGVWIR	10	HBV	adv	CORE	549	3.11	0.015	0.017			

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0007	FVCGPLTVNEK	10	HBV	sym	POL	698	3,11		0,0057	0,015		
1.0535	YYCPLTVNEK	10	HBV	adr	POL	669	3,11		0,0069	0,014		
1.1075	RLADEGLNRR	10	HBV	adr	POL	601	3,11		0,013	0,0004		
1.1086	IVKLKQCFR	10	HBV	adr	POL	1185	3,11		0,013	0,0024		
1.0773	PISSSWAFAK	10	HBV	adrw	ENV	314	3,11		<0,0003	0,010		
1.0778	LTVNENRRLK	10	HBV	adrw	POL	702	3,11		0,0025	0,0095		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.018	CTCCCSSDLY	9	HCV		LORF	1123	1	3.0	0	0	0.010	
1.012	NIVDVQLY	9	HCV		NS1/ENV2	697	1	0.60	0	0	0.010	
2.004	VQDNCNSY	9	HCV		302	1	0.54		0.005	0.003		
2.005	LTPRCMVY	9	HCV		605	1	0.078					
1.0145	RVCEKMAV	9	HCV		LORF	2588	1	0.053				
1.0140	DVCCCSMSY	9	HCV		LORF	2416	1	0.039				
2.0036	FTPKIRMY	9	HCV		636	1	0.012					
1.0509	GLSAFSLHSY	10	HCV		LORF	2888	1	0.41	0.0002	0.013	0.034	0.002
1.0499	TLHGQPTPLY	10	HCV		LORF	1617	1	0.30	0.11	0.024		
2.0037	EVVLLFLL	9	HCV			719	24				1.4	
2.0169	MIVGCCVHRL	10	HCV			633	24				0.026	
2.0170	EVVLLFLL	10	HCV			719	24				0.010	
1.0139	SVPAELRK	9	HCV		LORF	2269	3,11		0.016	0.57		
1.0953	QLPTESPR	9	HCV		ENV1	290	3,11		0.75	0.033		
1.0090	RIGVYATRK	9	HCV		CORE	43	3,11		0.74	0.16		
1.0123	LIRCHSKKK	9	HCV		LORF	1391	3,11		0.54	0.19		
1.0122	HURCHSKK	9	HCV		LORF	1390	3,11		0.23	0.010		
1.0952	KTSENSQPR	9	HCV		CORE	51	3,11		0.16	0.064		
1.0120	AVCTRCVAK	9	HCV		LORF	1183	3,11		0.016	0.038		
1.0143	EVRCVQPEK	9	HCV		LORF	2563	3,11		0.0019	0.033		
1.0137	ITRVESENK	9	HCV		LORF	2241	3,11		0.015	0.0079		
1.0957	CITSLIGR	9	HCV		LORF	1042	3,11		0.0095	0.011		
1.0496	CVAGALVARK	10	HCV		LORF	1858	3,11		0.57	1.1		
1.0480	HLLAFTPSCK	10	HCV		LORF	1227	3,11		0.57	0.0051		
1.1062	RMTVGGVERR	10	HCV		NS1/ENV2	632	3,11		0.77	0.012		
1.0485	HLLRCHSKKK	10	HCV		LORF	1390	3,11		0.77	0.025		
1.0484	TLGRCAYMSK	10	HCV		LORF	1261	3,11		0.17	0.13		
1.1067	CVGCVLLPNR	10	HCV		LORF	3002	3,11		0.0029	0.002		
1.1063	LFLFLLADAR	10	HCV		NS1/ENV2	723	3,11		0.015	0		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0014	PRDVYDVFY	9	HTV		CAG	298		1	0.090			
2.0129	IVQYMDLY	9	HTV		POL	875		0.064				
1.0028	TVLDVGDAY	9	HTV		POL	802		0.018	<0.0002	0.0056		
1.0012	TVVLDVGDAY	10	HTV		POL	801		0.28	0	0.0004		
1.0015	VIQYQYMDLY	10	HTV		POL	874		0.25	0.0007	0.0090		
2.0252	TVVLDVGDAY	10	HTV		POL	801		1	0.088			
1.0031	EVNIVTDQY	10	HTV		POL	1187		1	0.053			
1.0041	LVAVVHVASY	10	HTV		POL	1329		1	0.039			
1.0042	PAETGQETAY	10	HTV		POL	1345		1	0.013			
2.0251	ISKICPENY	10	HTV		POL	742		1	0.61	0.64		
2.0055	QMAVRIKDNFK	10	HTV		POL	1,432		3				
2.0064	RYLKQDQQL	9	HTV		POL	2,778		24				
2.0134	RYLKQDQQL	9	HTV		POL	2,778		24				
2.0065	TVQYQDQPF	9	HTV		POL	1,033		24				
2.0131	TVQYQDQPF	9	HTV		POL	1,033		24				
2.0063	TVQYQDQPL	9	HTV		POL	1,036		24				
2.0132	TVQYQDQPL	9	HTV		POL	1,036		24				
2.0066	TVQYMDLY	9	HTV		POL	875		24				
2.0247	TVKRWIILGL	10	HTV		POL	266		24				
2.0190	TVKRWIILGL	10	HTV		POL	266		24				
2.0249	TVPLASLISL	10	HTV		POL	506		24				
1.0059	KLACRWRWVK	9	HTV		POL	1358		3,11		2.7	0.069	
1.0044	AVFHNFKR	9	HTV		POL	1434		3,11	0.17	1.8		
1.0032	AIROSAMTK	9	HTV		POL	853		3,11	1.1	0.95		
1.0046	IVWGCCTPK	9	HTV		POL	1075		3,11	0.068	0.37		
1.0079	KLTEDRWNK	9	HTV		POL	1712		3,11	0.013	0.27		
1.0027	CPHPAGLK	9	HTV		POL	768		3,11	0.23	0.065		
1.0059	QIEQLIHK	9	HTV		POL	1215		3,11	0.0091	0.16		
1.0039	KWPSYKGR	9	HTV		CAG	443		3,11	0.12	0.0008		
1.0072	IIATDQTK	9	HTV		POL	1458		3,11	0.025	0.098		
1.0036	KGTELHPDK	9	HTV		POL	925		3,11	0.064	0.096		
1.0062	YLAWVPAHK	9	HTV		POL	1227		3,11	0.077	0.057		
1.0047	FWNTTPPLVK	9	HTV		CAG	443		3,11	0.077	<0.0005		
1.0024	NTTVVPAKK	9	HTV		POL	752		3,11	0.012	0.066		
1.0080	TVQCTHGIK	9	HTV		ENV	2420		3,11	0.0021	0.046		
1.0013	ILDIRQGPK	9	HTV		CAG	207		3,11	0.042	0.0048		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0015	RDVYVDRFK	9	HTLV		GAG	299	3.11			0.0007	0.040	
1.0058	GIQQAQFDK	9	HTLV		POL	1199	3.11			<0.0009	0.040	
1.0064	VLFQDGDK	9	HTLV		POL	1254	3.11			0.038	0.032	
1.0076	LVDRELNK	9	HTLV		POL	769	3.11			0.011	0.030	
1.0078	KVVPVRKAK	9	HTLV		POL	1513	3.11			0.029	0.039	
1.0042	MTKILEPFR	9	HTLV		POL	859	3.11			<0.0008	0.016	
1.0063	TVYVGVPVWK	10	HTLV		ENV	2185	3.11			3.8	7.8	
1.0018	TVQPIVLPK	10	HTLV		POL	935	3.11			0.16	5.6	
1.0047	AVFHINFKRK	10	HTLV		POL	1434	3.11			0.66	0.85	
1.0037	KVLFQDGDK	10	HTLV		POL	1253	3.11			0.36	0.70	
1.0008	KLVDFRELNK	10	HTLV		POL	768	3.11			0.51	0.090	
1.0003	KLKPGCMDCFK	10	HTLV		POL	706	3.11			0.39	0.076	
1.0095	FLCKIWPSTK	10	HTLV		GAC	440	3.11			0.32	0.024	
1.1056	KIONFRVYMR	10	HTLV		POL	1474	3.11			0.022	0.21	
1.0010	GIPHPAGLKK	10	HTLV		POL	788	3.11			0.011	0.17	
1.0026	LVKLWYQLEK	10	HTLV		POL	1117	3.11			0.066	0.082	
1.0036	MIGGICGFK	10	HTLV		POL	642	3.11			0.0099	0.053	
1.0013	MTKILEPFRK	10	HTLV		POL	859	3.11			0.015	0.038	
1.0053	WQDQNSDK	10	HTLV		POL	1504	3.11			<0.0005	0.021	
1.0094	FLCKIWPSTK	10	HTLV		GAC	440	3.11			0.020	0.0013	
1.1059	MQQONNLLR	10	HTLV		ENV	2741	3.11			0.0024	0.019	
1.0017	HTPPDKKHOK	10	HTLV		POL	909	3.11			<0.0002	0.015	
1.0005	LVEICTEMER	10	HTLV		POL	729	3.11			0.0002	0.012	
1.0092	LWQNANPDK	10	HTLV		GAC	327	3.11			<0.0002	0.011	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0225	ISETRHRHCV	9	HPV	16	E6	80	1	78	—	0.0011	0.036	—
1.0230	QAEFDRAINY	9	HPV	16	E7	44	—	0.021	—	<0.0002	<0.0002	—
1.0610	LCQIEETTCVY	10	HPV	16	E6	25	—	0.25	—	0.0056	0.012	—
2.0159	YSKISERHY	10	HPV	16	E5	77	—	0.17	—	<0.0009	0	—
2.0162	YSKISERHY	10	HPV	16	E6	77	—	0.11	—	<0.0009	0	—
1.0599	HCDIPTLHEY	10	HPV	16	E7	2	—	0.087	—	<0.0002	<0.0002	—
1.0601	QETTDILYCY	10	HPV	16	E7	16	—	0.033	—	—	—	—
1.0913	ILHIDILECVY	10	HPV	16	E6	30	—	0.033	—	—	—	—
1.0594	AVCDKCLKY	10	HPV	16	E6	64	—	0.0095	—	0.0052	0.019	—
2.0160	YSRIREHLRY	10	HPV	18	E6	72	1	0.018	—	<0.0002	<0.0002	—
2.0164	YSRIREHLRY	10	HPV	18	E6	72	1	0.012	—	—	—	—
2.0161	LLRCLCLCOK	10	HPV	18	E5	101	3	—	0.061	0.078	—	—
2.0032	HTMLLCMKCK	9	HPV	18	E7	59	11	—	0.020	0.079	—	—
2.0029	VRCKTVLRL	9	HPV	18	E6	33	24	—	—	—	0.33	—
2.0027	CYSLYGTTL	9	HPV	16	E5	57	24	—	—	—	0.057	—
2.0024	YTDRAARDL	9	HPV	16	E5	49	24	—	—	—	0.032	—
2.0031	LVNLLRCL	9	HPV	18	E5	98	24	—	—	—	0.019	—
2.0030	VRGDNLECL	9	HPV	18	E6	85	24	—	—	—	0.010	—
1.0239	SYNGDNLEK	9	HPV	18	E6	84	3,11	—	0.399	2.3	—	—
1.0243	SYNGDNLEK	9	HPV	18	E5	84	3,11	—	0.35	1.1	—	—
1.0244	SYNGDNLEK	9	HPV	18	E6	84	3,11	—	0.70	0.95	—	—
1.0226	TTLEQQQNK	9	HPV	16	E6	93	3,11	—	0.010	0.67	—	—
1.0241	SIPHAACHK	9	HPV	18	E5	59	3,11	—	0.0094	0.25	—	—
1.0237	SIPHAACHK	9	HPV	18	E5	59	3,11	—	0.017	0.12	—	—
1.0233	TCIPRCOK	9	HPV	16	E7	89	3,11	—	0.035	0.023	—	—
1.0597	KLRHLNEKRR	9	HPV	18	E6	117	3,11	—	0.025	<0.0005	—	—
1.0234	URCLCLCOK	9	HPV	18	E6	102	3,11	—	0.019	0.0012	—	—
1.0853	ILIECVLCK	9	HPV	16	E5	33	3,11	—	0.0016	0.019	—	—
1.0599	CIDPFSRIR	9	HPV	18	E6	68	3,11	—	0.017	0.0018	—	—
1.0598	CIDPFSRIR	9	HPV	18	E6	68	3,11	—	—	—	—	—
1.0629	LLRCLCLCOK	10	HPV	18	E6	101	3,11	—	0.16	0.11	—	—
1.0614	LTEVFEFAFK	10	HPV	18	E6	41	3,11	—	0.0009	0.11	—	—
1.0605	GVCPICSQK	10	HPV	16	E7	88	3,11	—	0.0017	0.060	—	—
1.0625	LTEVFEFAFK	10	HPV	18	E6	41	3,11	—	0.0012	0.041	—	—
1.0591	DILECVYCK	10	HPV	16	E6	32	3,11	—	0.0065	0.021	—	—
1.1101	KLRHLNEKRR	10	HPV	18	E6	117	3,11	—	0.013	0	—	—
1.1095	CYCKQQLR	10	HPV	16	E6	37	3,11	—	0.011	0.0059	—	—

Pepidpe	Sequence	AA	Virus	Strain	Molecule	Pos.	Molif	A1	A2.1	A3.2	A11	A24
2.0070	EVDPGCHLY	9	MACE	3		161	1	18	0.0002	0.0002		
3.0177	EVDPGCHLY	9	MACE	5/51		161	1	9.9	0.0006	0.0006	0	
1.0259	TQDQWQKTY	9	MACE	1		240	1	21	0	0.0002		
3.0173	EVDPGCHLY	9	MACE	6		161	1	1.9	0.0002	0.0002	0	
1.0254	EVDPGCHLY	9	MACE	1		161	1	1.1	0	0	0	
1.0259	LVDPGCHLY	9	MACE	1		240	1	0.42	0.0013	0.005		
4.0053	TSVWVKEY	9	MACE	1		new	275	1	0.099			
2.0009	SELPVTVTY	9	MACE	3		9	1	0.05				
2.0111	GSVVGWVWY	9	MACE	3		77	1	0.050				
2.0008	SELPVTVTY	9	MACE	2		9	1	0.043				
1.0253	MLESVWVY	9	MACE	128		1	0.011					
2.0147	ASPLVTVTY	10	MACE	3		8	1	24	0.0009	0.003		
2.0167	LTDQDQVQY	10	MACE	1		239	1	1.2	0.0009	0.0072		
4.0114	EVISPVVLY	10	MACE	1		new	274	1	0.56			
2.0141	ASPLVTVTY	10	MACE	2		9	1	0.17	0.0009	0.001		
1.0248	QWVQVKEY	10	MACE	1		242	1	0.04				
4.0048	TSVWVKEY	9	MACE	new		275	3		0.71	0.570		
4.0114	EVISPVVLY	9	MACE	66		3			0.003	0.07		
4.0114	EVISPVVLY	9	MACE	new		277	3		0.31	0.34		
4.0114	EVISPVVLY	9	MACE	new		278	3		0.0009	0.11		
4.0132	LTDQDQVQY	9	MACE	239		3			0.0026	0.004		
4.0083	LVDPGCHLY	9	MACE	new		243	3		0.0009	0.0009		
4.0131	EVISPVVLY	9	MACE	239		3			0.004	0.0009		
4.0132	EVISPVVLY	9	MACE	97		3			0.011	0.0005		
4.0124	EVISPVVLY	10	MACE	new		260	1					
4.0161	ADPGVCHLY	10	MACE	107		3			0.35	0.29		
4.0140	EVISPVVLY	10	MACE	95		1			0.14	0.006		
4.0119	EVISPVVLY	10	MACE	242		3			0.002	0.005		
4.0123	EVISPVVLY	10	MACE	new		263	3		0.019	0.0009		
4.0164	LSVWVKEY	10	MACE	218		3			0.0009	0.011		
4.0149	KABDLSVWY	10	MACE	123		3			0.0009	0.0009		
4.0125	KABDLSVWY	10	MACE	1		new	270	11	0.18	0.24		
2.0010	NTPLWVQY	9	MACE	3		16	24				0.077	
2.0168	NTPLWVQY	10	MACE	125		24					0.25	
1.1104	TTTNPVQY	9	MACE	1		115	24					
2.0151	LYTATDGL	10	MACE	3		239	24					
4.0124	STKVKVLY	10	MACE	1		new	276	24				
1.0249	SLSPLAVTK	9	MACE	1		96	3.11		4.1	2.7		
1.1103	SYMPVYDQ	9	MACE	1		219	3.11		0.0003	1.1		
1.1104	TTTNPVQY	9	MACE	1		66	3.11		0.006	1.0		
1.0257	LTDQDQVQY	9	MACE	1		239	3.11		0.0002	0.34		
1.0244	SLSPLAVTK	10	MACE	1		96	3.11		1.7	0.9		
1.0247	LTDQDQVQY	10	MACE	239		3.11			0.004	0.16		
1.0240	MLESVWVY	10	MACE	1		239	3.11		0.14	0.07		
1.0244	LLGDNQWPK	10	MACE	1		102	3.11		0.020	0.011		
1.0230	SLSPLAVTK	10	MACE	1		7			0.015	0.015		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A.1	A.2.1	A.3.2	A.11	A.24
1.0261	CSNDCTTIVY	9	p53			226	1	29.5		0.0010	0.079	
1.0667	CTAKSVTCTY	10	p53			117	1	0.33	0	0.023	0.049	0
1.0672	RVEGNLRLVEY	10	p53			196	1	0.022		0.0014	0.0020	
1.0778	RVRAMAYK	9	p53			156	3,11			1.5	0.73	
1.0776	CTYSPANK	9	p53			124	3,11			0.46	1.1	
1.0785	NTSSSRQPK	9	p53			311	3,11			0.0009	0.005	
1.0264	RTEENRK	9	p53			283	3,11			0.0018	0.091	
1.0267	ELNEALELK	9	p53			343	3,11			0.020	0.0052	
1.0678	RTEEDNLRK	10	p53			283	3,11			3.3	0.0080	
1.1113	KTVQGSYGR	10	p53			101	3,11			2.6	0.88	
1.1115	VVRCPHHER	10	p53			172	3,11			0.0099	0.0017	
1.0679	NTSSSRQPK	10	p53			311	3,11			0.005	0.064	
1.1121	RVCACCPGRDR	10	p53			273	3,11			0.014	0.011	
1.1116	GLAPPROHLR	10	p53			187	3,11			0.013	0.0006	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
3.075	KCEYFVEMY	9	PAP			322	1	3.4		<0.0002	0.0002	0
3.074	LCYMRKRY	9	PAP				81	1	0.78	<0.0002	0.0002	0
3.076	ASCHILTELY	9	PAP				311	1	0.77	<0.0002	<0.0002	0.055
3.073	ESYKHEQVY	9	PAP				95	1	0.098	<0.0002	0.0002	0
3.077	LSLSLSLISLY	10	PAP				238	1	14	0.0026	0.0004	0
3.075	LSLSLSLISLY	10	PAP				238	1	12	0.0008	0.0004	0
3.076	LTQLCMEQHY	10	PAP				70	1	0.62	0.0005	0.015	0.0024
3.073	KCEYFVEMY	10	PAP				322	1	0.018	0.0057	0.089	
3.070	LWNEILNHMK	10	PAP				263	3		0.066	0.12	
3.058	ATQIISYKK	9	PAP				274	11		0.10	1.2	
3.071	ETLQKSEEPQK	10	PAP				170	11		<0.0004	0.014	
3.071	LYFEKGEYP	9	PAP				318	24			2.5	
3.070	LYCESVHNIF	9	PAP				213	24			0.44	
3.079	PKYDPRATL	9	PAP				163	24			0.11	
3.072	YVNGLLIPY	9	PAP				302	24			0.032	
3.072	PTASCHLTEL	10	PAP				309	24			0.024	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Modif	A1	A3.2	A11	A26
1.0270	ALPERDIFLY	9	PSA			233	1	0.011			
2.0337	VSHSHPHFLY	10	PSA			69	1	0.15	-0.0003	0.003	
1.0285	FLYOMBALK	9	PSA			65	1.11		0.24	0.057	
1.0273	VVWVYKWK	9	PSA			242	1.11		0.0072	0.003	
1.0272	YTKVVVHYK	9	PSA			249	1.11		0.0038	0.008	
1.1639	SLIIONTRPLR	9	PSA			169	1.11		0.0004	0.007	
1.0280	IVGCCWECIK	9	PSA			21	1.11		0.011	0.019	
1.0289	QVWYQKVTE	9	PSA			182	1.11		0.0009	0.014	
1.1133	SLYTKVVVWYR	10	PSA			227	1.11		0.28	0.23	
1.0263	LTAAMHCENK	10	PSA			57	1.11		0.14	0.003	
1.0261	IVGCCWECIK	10	PSA			20	1.11		0.004	0.007	
1.0262	KVVWVYKWK	10	PSA			241	1.11		0.005	0.005	
1.1111	YTKVPALEACK	10	PSA			180	1.11		0.0003	0.013	
3.0108	MUUELSEPA	9	PSA			118	1.11				

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
EDTPIGHLY	9	MAGE3 _a	3	analog		161	A01	12.5000			
AVDPIGHLY	9	MAGE3 _a	3	analog		161	A01	8.0000			
EVDPIGHLY	9	MAGE3 _a	3	analog		161	A01	5.5000			
PSPAPDNLYY	10	HER-2/neu				1213	A01	5.5000	0.0005	0.0010	
EVDAIGHLY	9	MAGE3 _a	3	analog		161	A01	5.3500			
EVDPIGHLY	9	- MAGE3 _a	3	analog		161	A01	5.0000			
EVDPIGHAY	9	MAGE3 _a	3	analog		161	A01	4.6500			
EADPIGHLY	9	MAGE3 _a	3	analog		161	A01	3.4500			
EVDPIGHLY	9	MAGE3 _a	3	analog		161	A01	2.9500			
EVDPIGHSY	9	MAGE3 _a	3	analog		161	A01	2.6667			
EVDPIGHLY	9	MAGE3 _a	3	analog		161	A01	2.4000			
EVDPASNTY	9	MAGE	4			161	A01	1.5000			
PLSEDQQLY	9	PAP				147	A01	1.2000	0.0005	0.0001	
LSAFSLHSY	9	HCV				2889	A01	0.8100	0.0002	0.0002	
IPSYKKLIMY	10	PAP				277	A01	0.5650			
YASCHLTEL	10	PAP				310	A01	0.5467	0.0003	0.0002	
EVDPIGHLA	9	MAGE3 _a	3	analog		161	A01	0.3300			
CHQIAKGM SY	10	HER-2/neu				826	A01	0.2967	0.0003	0.0001	
VGSDCTTIHY	10	P53				225	A01	0.2600	0.0003	0.0003	
EVAPIGHLY	9	MAGE3 _a	3	analog		161	A01	0.1800			

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq.	Pos.	Motif	A01	A03	All	A24
							Bind.	Bind.	Bind.	Bind.	Bind.
ESMPNPZCHY	10	HER-2/neu			280	A01	0.1800	0.0003	0.0003		
ASCVTACPY	9	HER-2/neu			293	A01	0.0552	0.0008		0.0074	
PSPAFDNY	9	HER-2/neu			1213	A01	0.0125	0.0002	0.0002		
ASPLDSDTPY	9	HER-2/neu			997	A01	0.0290	0.0002	0.0004		
RGTQLFENDY	10	HER-2/neu			103	A01	0.0205	0.0003	0.0015		
PASPLDSDTPY	10	HER-2/neu			996	A01	0.0148	0.0003	0.0001		
PSQKTYQQSY	10	P53			98	A01	0.0140	0.0003	0.0003		
KSTKVPAY	9	HCV			1236	A01	0.0134	0.0009	0.0001		
DSSVLCBCY	9	HCV			1513	A01	0.0110	0.0002	0.0003		
KISBYKHYTCY	10	HPV	16	E6	79	A01	0.0090	0.0043	0.0038		
NLYVSIHLILY	10	HBV	adv	POL	20	1088	A01	0.0090			
GTRVRAAMAY	10	P53			154	A01/03	0.0027	0.0365	0.0002		
LTCGFADLMGY	11	HCV			126	A01/11	2.4500	0.0003	0.0120	0.0001	
VHAGVCSPY	9	HER-2/neu			773	A01/A03	0.0400	0.0575	0.0079		
TLWKGAGILY	9	HBV	adr	POL	100	724	A03	0.0017	0.2667	0.0016	
KLNWASQIY	9	HIV		POL		958	A03	0.0070	0.1160	0.0006	
LVGFLILKY	9	MAGE1	1			109	A03	0.0033	0.0563	0.0012	
ILRGTTSFVY	9	HBV	adr	POL	80	1345	A03	0.0017	0.0440	0.0002	
RVVQGLPREY	10	HER-2/neu			545	A03	0.0015	0.0350	0.0050		

Table 5

Sequence	Site	Antigen	Strain	Molecule	Freq.	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
QLVTQLMFY	9	HER-2/neu			795	A03	0.0024	0.0112	0.0039		
CLNKIVRY	9	HIV		GAG	274	A03	0.0017	0.0103	0.0002		
LLGDNQVMPK	10	MAcE2	2		182	A03		0.0093	0.0014		
QVRDQAEHLK	10	HIV		POL	1419	A03		0.0089	0.0093		
LVSAGIRK	8	HIV	con		1246	A03		0.0091	0.0054		
VTDRGRQK	8	HIV	con		1153	A03		0.0090	0.0065		
TVFDAKRLIGR	11	HLA-Aw68 endogenous peptide sequences				A03/11		0.1050	1.3000		
KTGGPIYKR	9	HLA-Aw68 endogenous peptide sequences				A03/11		0.0340	0.8200		
SLYTKVVHY	9	PSA			237	A03/11	0.0017	0.6750	0.0140		
AVAAVARR	9	HLA-Aw68 endogenous peptide sequences				A03/11		0.1600	0.0825		
KIQNPRVY	9	HIV		POL	1474	A03/11	0.0056	0.1190	0.1350		
EALESVIKVK	11	MAcB1			127	A03/11		0.0087	0.0099		
EVAPPETYHRK	10	HLA-Aw68 endogenous peptide sequences				A11		0.0008	0.0575		
ETAXFLK	8	HIV	consensus		1351	A11		0.0037	0.0425		
RWGLLALL	9	HER-2/neu			8	A24			1.2567		
PYVSRLGI	9	HER-2/neu			780	A24			0.1650		
VTMIMKCKW	9	HER-2/neu			951	A24			0.1640		
AYSLLTQLGL	9	HER-2/neu			440	A24			0.1250		
SYGVTWEL	9	HER-2/neu			907	A24			0.1200		
LYISAMPDSL	10	HER-2/neu			410	A24			0.0835		
VMSYGVTVW	9	HER-2/neu			905	A24			0.0800		

Table 5

Table 5

Sequence	Mag strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DLVGFLLK	9	1	108	3,11		0.0040	0.0014		
QLVFGIDVK	9	1	152	3,11		0.0019	0.0051		
SLEQRSLHCK	10	1	2	3,11		0.015	0.015		
SLFRAVITKK	10	1	96	3,11		1.2	0.98		
DLYGELLKX	10	1	108	1	0.0068	0.0009			
MLESVTIVKX	10	1	128	3,11		0.14	0.027		
WEEELSVLEVY	10	1	215	1	<0.0009	<0.0002	<0.0002		
VYDGDREHSSAY	10	1	223	1	<0.0009				
LYGFLLLKX	9	1	109	1	0.0033	0.056	0.0012		
LYTCGLGSY	9	1	171	1	0.0084	0.0014	<0.0002		
VLVTCGLGSY	10	1	170	1	0.0048	0	0.0013	0.0007	
FLLKRYAR	9	1/2/3	112	3,11		0.0007	<0.0005		
PTTINPFRQR	10	1	65	3,11		<0.0002	0.0033		
LVGGFLLLKRY	10	1	109	3,11		0.0034	0.0023		
EKYLEYGRCR	10	1	246	3,11		<0.0002	0		
ELVHFLLK	9	2/3	108	3		0.0045	0.0011		
AYGEPKLL	9	1	231	24				0.0007	
SIVLVTCGL	10	1	168	24		0.0006		0.0051	
EVVPISHLY	9	2	161	1	0.0028	<0.0002	<0.0002		
EVVIGHLY	9	21	161	1	0.0002				
EVDPASNTY	9	4	161	1	0.0005				
EADPSTSNTY	9	5/51	161	1	9.9	0.0006	0.0006	0	

Table 5

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
EVDPIGHVY	9	6		161	1	1.9		<0.0002	<0.0002	0
ENLIESVIK	8	1		127	3			<0.0003	0	
LYFGIDVK	8	1		153	3			0.0035	0.0037	
GYQGQPSLK	8	1		266	3			<0.0003	0.0063	
YMEYVYDGR	8	1		220	3			<0.0003	0.0007	
VQEKYLEY	8	1		244	1	0.0018				
VKEADPTCHSY	11	1		231	24					0.0017
AYGIEPRKL	8	1		159	1	<0.0003				
IWEELLSVMEVT	11	1		214	1	<0.0003				
ENLIESVIKVK	11	1		127	3		0.0087	0.0099		
EADPTSHTY	9	analog		161	1	0.68				
EVDPTSNTY	9	analog		161	1	1.6				
EALEAQQA	9	1		14	2.1	0	<0.0002	0		
HSLEQRLH	9	1		1	3			0.0025	0.0003	
QSPQQASAF	9	1		56	3			0.0004	0	
SARFTTINP	9	1		62	3			<0.0003	0	0.0003
TSCILESFL	9	1		90	3			<0.0003	0	
SCILESFLR	9	1		91	3			<0.0003	0.0026	
LFRAVITKK	9	1		97	3			0.011	0.0005	
VGFLLLKVR	9	1		110	3			0.0044	0.0051	
ZSVIKVYKH	9	1		130	3			<0.0003	0	
VIKVKVKCP	9	1		132	3			<0.0003	0	

Table 5

Sequence	AA strain	Mass Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
ASSESIQIYF	9 1,2		147	3			<0.0003	0	
LGDNQIIMPK	9 1		183	3			0.0007	0.0048	
WLMIAEQGH	9 1		200	3			<0.0003	0	
YDGGRHHSAY	9 1		224	3			<0.0003	0	
LTDQDVQEK	9 1		239	3			<0.0003	0.14	
CGVQGQPSLK	9 1		265	3			<0.0003	0.0037	
EMLESVIKY	10 1		127	1	0.0006		<0.0002	<0.0002	0
KEDADPTQHSY	10 1		160	1	<0.0005		<0.0002	<0.0002	
ASAPPTTINP	10 1		61	3			<0.0003	<0.0002	
APPTTINPTR	10 1		63	3			<0.0003	0.0003	
PTTINPTQR	10 1		65	3			<0.0003	0.0002	
STSCILESILP	10 1		89	3			<0.0003	<0.0002	
GFLLLKRYRAR	10 1		111	3			0.0019	0.0008	
KAEMLESVIK	10 1		125	3			<0.0003	0.0097	
SVIKNYKHCF	10 1		131	3			<0.0003	<0.0002	
KASESIQIYF	10 1		146	3			<0.0003	<0.0002	0.0012
DVKEDADPTCH	10 1		158	3			<0.0003	<0.0002	
LWMIAEQGH	10 1		199	3			0.0008	0.0005	
LSVMAFVYDGR	10 1		218	3			<0.0003	0.012	
VMEVYDGREH	10 1		220	3			<0.0003	0.0002	0
YGRCRTVIPH	10 1		251	3			<0.0003	<0.0002	
SCGVQGQPSLK	10 1		264	3			0.0005	0.0089	

Table 5

Sequence	AA	Mage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VPDSDPARY	9	1	new	254	1	0.0038				
QVPDSDPARY	9	1	new	254	3		<0.0003	0.0002		
VIKVSVRVR	9	1	new	284	3		0.0016	0		
PSLREAAIR	9	1	new	296	3		<0.0003	0		
EFLWGPRAL	9	1	new	264	24				0.0006	
ETSYVTKVLEY	10	1	new	274	1	0.56				
LVQEKKYLEYR	10	1	new	243	3		0.0008	0.0043		
QVPDSDPARY	10	1	new	254	3		0.0014	0.0003		
YVKVLEYVIK	10	1	new	277	3		0.0029	0.0015		
YVIKVSVRVR	10	1	new	283	3		0.019	0.0009		
RALAEETSYVK	10	1	new	270	11		0.18	0.24		
SYVKVLEYVI	10	1	new	276	24				0.036	
PPPSLREAL	10	1	new	294	24				0.0044	
SVIKNYK	7	1 N	POL	131	3,11		0.0006	0.0028		
PVTKAEMLESVIK	13	1 n	E6	122	3,11		<0.0003	0		
ETSYVVKVLEYVIK	13	1 n	E6	273	3,11		0.0044	0.0003		
ITKKVADLVGFLLK	15	1 n	POL	102	3,11		0.40	1.0		
VTKAEMLESVIKVK	15	1 n	POL	123	3,11		0.024	0.053		
VVGNWQYPPVIPSX	15	3	POL	79	3,11		1.6	0.34		
PRALAEETSY	9	1	new	268	1	<0.0018	<0.0003	<0.0002		
FATCLGLSX	9	3		171	1	0.038	<0.0003	0.0004		
LEQRLSLHCK	9	1	new	3	3		<0.0002	0		

Table 5

Sequence	AA	Wage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AEMLESVIK	9	1	new	126	3		<0.0002	0.0011		
LESVIKNYK	9	1	new	129	3		<0.0002	0.0018		
EELSVMEVY	9	1	new	216	3		<0.0002	0		
MEVYDGREH	9	1	new	221	3		<0.0002	0		
DSDPARYEP	9	1	new	256	3		<0.0002	0		
KVSGARVRPP	9	1	new	285	3		0.0005	0		
VSARVRPPP	9	1	new	286	3		0.0003	0.0026		
HSPQGASSF	9	2		56	3		<0.0002	0		
TTINTYTLWR	9	2		66	3		0.089	1.1		
QEEEGPRMP	9	2		83	3		<0.0002	0		
MFPDQLESEP	9	2		90	3		<0.0002	0	0.014	
SEFQMAISR	9	2		96	3		<0.0002	0.0001		
EFQMAISRK	9	2		97	3		<0.0002	0.0002		
LVHFLILKX	9	2,3		109	3		0.043	0.010		
AEMLESVLR	9	2		126	3		<0.0002	0		
SVLFLNCQDF	9	2		131	3		<0.0002	0		
VLRNCQDF	9	2		132	3		<0.0002	0		
DFFFVYIFSK	9	2		138	3		<0.0002	0.0022		
VIPSEASEY	9	2		142	3		0.081	0.033		
VIVEVYPISH	9	2		159	3		0.0007	0.010		
LGDNQVAPK	9	2		183	3		<0.0002	0.0061		
EGDCAPEEK	9	2,3		205	3		<0.0002	0		

Table 5

Sequence	AA	Wage	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QEEECPSTR	9	3		83	3				<0.0002	0	
TPPDLESEF	9	3		90	3				<0.0002	0	0.0049
SEFQALSLR	9	3		96	3				<0.0002	0	
EPQQALSRK	9	3		97	3				<0.0002	0.0001	
SVVGNWQYF	9	3		131	3				<0.0002	0	
WVGDNWQYF	9	3		132	3				0.0022	0.0021	
YPPPVIPSK	9	3		138	3				0.0020	0.027	
ASSSLQLVF	9	-	3	147	3				0.0011	0.0089	
LHEVDPIGH	9	3		159	3				<0.0002	0	
IIVLAIARI	9	3		196	3				0.0069	0.0011	
VQEKYLEYR	9	1		244	11				<0.0002	0	
SNQEEEGPR	9	2		81	11				<0.0002	0	
NYKHCPEI	9	1	new	135	24					4.8	
IFGKASESL	9	1	new	143	24					0.0013	
GFLLIVLVM	9	1	new	193	24					<0.0002	
IFSKASEYL	9	2		143	24					0.023	
EYLQLVFGI	9	2		149	24					3.5	
NWQIYFPVI	9	3		135	24					0.53	
IPSKASSL	9	3		143	24					0.016	
LSQVGNWQY	10	3		129	1	<0.0020			<0.0003	0.0012	
IPATCQLSY	10	3		170	1	<0.0002			0.0005	0.0004	
TSCLLESLFR	10	1	new	90	3				<0.0002	0.015	

Table 5

Sequence	AA	Mass strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
LESVIKNYKH	10	1	new	129	3			<0.0002	<0.0002	
REHSAVGEPR	10	1	new	227	3			<0.0002	<0.0002	
PDSDPARYEF	10	1	new	255	3			<0.0002	<0.0002	
LEYVIKVSAR	10	1	new	280	3			<0.0002	<0.0002	
VIKVSARVRF	10	1	new	283	3			<0.0002	<0.0002	
XVSARVRFFF	10	1	new	285	3			0.0013	0.0020	
STTINYTLWR	10	2		65	3			0.0014	0.091	
SSNQEEEGPR	10	2		80	3			<0.0002	<0.0002	
RHPPDLESEP	10	2		89	3			<0.0002	<0.0002	0.0016
ESEFQAAISR	10	2		95	3			<0.0002	<0.0002	
SEFQAAISRK	10	2		96	3			0.0012	0.0028	
ISRKMKVELVH	10	2		102	3			<0.0002	<0.0002	
VELVHFLLK	10	2		107	3			0.0009	0.0003	
ELVHFLLKY	10	2,3		108	3			0.0066	0.0003	
LVHFLLKRY	10	2		109	3			0.026	0.0022	
HFLLKRYAR	10	2,3		111	3			0.0014	0.0002	
KAEKMLESVLR	10	2		125	3			<0.0002	0.0009	
ESVLRNCQDF	10	2		130	3			<0.0002	<0.0002	
SVLRLNCQDFP	10	2		131	3			<0.0002	<0.0002	
NCQDPFPVIF	10	2		135	3			<0.0002	<0.0002	
QDFFPVIFSK	10	2		137	3			<0.0002	0.0083	
PVIFSKASEY	10	2		141	3			0.016	0.0033	

Table 5

Sequence	AA	Residue String	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KASEYVQLVY	10	2		146	3			<0.0002	<0.0002	0.0030
EVVEVVPISH	10	2		158	3			<0.0002	<0.0002	
VEVVPISHLY	10	2		160	3			<0.0002	<0.0002	
ILVTCGLSY	10	2		170	3			0.0036	0.0002	
LLGDNQVMPK	10	2		182	3			0.0093	0.0014	
IEGDCAPEEK	10	2		204	3			<0.0002	<0.0002	
STFPDLESEF	10	3		89	3			<0.0002	<0.0002	
ESEFQALSR	10	3		95	3			<0.0002	<0.0002	
SEFQALSRK	10	3		96	3			0.0010	0.0010	
LSRKVAELVH	10	3		102	3			<0.0002	<0.0002	
AELVHPLLK	10	3		107	3			0.0008	<0.0002	
LVHPLLKYR	10	3		109	3			0.040	0.0014	
GSVVGWNQYF	10	3		130	3			0.0020	0.0008	
SVVGWNQYFF	10	3		131	3			0.0085	0.0067	
KASSSLQLVF	10	3		146	3			0.0003	0.0008	0.0021
ELMEVDPIGH	10	3		158	3			<0.0003	<0.0002	
MEVDPIGHLY	10	3		160	3			0.0004	0.0004	
VDPIGHLYIF	10	3		162	3			<0.0003	<0.0002	
LIIVLAAIAR	10	3		195	3			0.028	0.0021	
REGDCAPEEK	10	3		204	3			<0.0003	<0.0002	
RQPSGESSSR	10	1	new	74	11			0.0009	0.0009	
LQLVFGIDVK	10	1	new	151	11			0.0050	0.0018	

Table 5

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
RQVPDSDPAR	10	1	new	252	11			<0.0003	<0.0002	
MNYPLWSQSY	10	3	new	68	11			<0.0003	<0.0002	
GFLILIVLVM	10	1	new	193	24					0.0008
SPSTTINYTL	10	2		63	24					0.015
EPQAAISRKW	10	2		97	24					<0.0002
LYILVTCGL	10	2		168	24					0.014
MWQYPPPVIF	10	3		135	24					0.017
AVDPIGHLY	9	-	3	analog	161	1	8.0			
EADPIGHLY	9	3	analog	161	1	3.5				
EVDPASNTY	9	4		161	1	1.5				
EDTPIGHLY	9	3	analog	161	1	13				
EVDPTGHLY	9	3	analog	161	1	3.0				
ADDSPSPPH	9	2		55	A11					
VPISHLYIL	9	2		170	P1					
HPKTRGLLII	9	2		196	P1					
SMLGVFEGR	9	2		226	A11					
DSVPFAHPRK	9	2		236	A11					
VPAHPRKLL	9	2		238	A24					
MDLVQENY	9	2		247	A01					
DPACYEFILW	9	2		265	P2					
FLWQPRALI	9	2		271	A02					
ALIETSYVK	9	2		277	A03/A11					

Table 5

Sequence	AA	Wage strain	Wol.	Pos.	Notif	A1	A2.1	A3.2	A11	A24
TSYVKVLHH	9	2		281	A11					
EPHISYPPPL	9	2		296	P1					
ISYPPPLHER	9	2		299	A03/A11					
YPPPLHERAL	9	2		301	P1					
EPVTKAEML	9	2/3		128	P1					
VPGSDPACY	9	2/3		261	P2					
EGCLEARGEA	9	3		14	A03					
CLEARGEAL	9	3		15	A02					
EARGEALGL	9	3		17	A02					
ALGLVGAQQA	9	3		22	A02/A03					
GLVGAQQA	9	3		24	A02/A03					
LVGAQQA	9	3		25	A02					
PATEQEAA	9	3		31	A02/A03					
EAASSSSTL	9	3		37	A02					
AASSSSTLV	9	3		38	A02					
LVEVTLGEV	9	3		45	A02					
EVTLGEVPA	9	3		47	A02/A03					
VTLGEVPA	9	3		48	A02/A03					
LPTTMNYPL	9	3		71	P1					
PDLESEFQAA	9	3		99	A03					
HPLLKYRA	9	3		118	A03					
PPPVIPSKA	9	3		146	A03					

Table 5

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DPICHLYIF	9	3		170	P2					
GDNQIMPKA	9	3		191	A03					
MPKACLLII	9	3		196	P1					
AGLLIIVLA	9	3		199	A03					
KIWEELSVL	9	3		220	A02					
SVLEVPEGR	9	3		226	A03/A11					
EDSILGDPK	9	3		235	A03/A11					
SILGDPKKL	9	3		237	A02					
ILGDPKKL	9	3		238	A02					
FLWGPRALV	9	3		271	A02					
PRALVETSY	9	3		275	A01					
RALVETSYV	9	3		276	A02					
ALVETSYVK	9	3		277	A03/A11					
LVETSYVKV	9	3		278	A02					
YVKVLHHHV	9	3		283	A02					
KVLHHHVVKI	9	3		285	A02					
MVKISGGPH	9	3		290	A03/A11					
ISGGPHISX	9	3		293	A01/A03/A11					
GPHISYPPL	9	3		296	P1					
YPPLHEWVL	9	3		301	P1					
VPISHLYILV	10	2		170	P1					
MPKTGLLIV	10	2		196	P1					

Table 5

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VFEGREDSVT	10	2		230	A24					
HPRKLIMQDL	10	2		241	P1					
LMQDLVQENY	10	2		246	A01					
EPLWQPRALI	10	2		270	A24					
CPRALIETSY	10	2		274	P2					
RALIETSYVK	10	2		276	A11					
SYVKVLHHHTL	10	2		282	A24					
SYPPHLERAL	10	- 2		300	A24					
APEEKIWEEL	10	2/3		216	P1					
PLEQRSQHCK	10	3		2	A03/A11					
HCKPKEEGLEA	10	3		9	A03					
EARGEALGLV	10	3		17	A02					
RGEALGLYGA	10	3		19	A03					
EALGLYGAQA	10	3		21	A02/A03					
LGLVGAQAPA	10	3		23	A03					
GLVGAQAPAT	10	3		24	A02					
QAPATEEEQEA	10	3		29	A02/A03					
EAASSSSSTLV	10	3		37	A02					
TLVETLGEV	10	3		44	A02					
EVTLGEVPA	10	3		47	A02/A03					
PDPPQSPQGA	10	3		59	A03					
LPTTNNYPLW	10	3		71	P2					

Table 5

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PDLESEPOAA	10	3		99	A03					
YPPPViPSKA	10	3		145	A03					
LGDNQIMPKA	10	3		190	A03					
MPKAGGLLIV	10	3		196	P1					
EVPGEGREDSI	10	3		229	A02					
EDSILGDPKK	10	3		235	A03/A11					
SILGDPKKL	10	3		237	A02					
ILGDPKKLIT	10	3		238	A02					
GDPKULLTQH	10	3		240	A03/A11					
DPKKULLTQHF	10	3		241	P2					
LTOQHFFQENY	10	3		246	A01/A03/A11					
PVQENYLEYR	10	3		250	A03/A11					
ACYEPLWQPR	10	3		267	A03/A11					
GPRALVETSY	10	3		274	P2					
RALVETSYVK	10	3		276	A03/A11					
ALVETSYVKV	10	3		277	A02					
LVETSYVKVL	10	3		278	A02					
YVKVLHHMK	10	3		283	A03/A11					
MVKISCCPHI	10	3		290	A02					
KISGGPHISY	10	3		292	A01					
SPPHISPGCA	9	2		60	P2A					
APATEEQEA	9	3		30	P2A					

Table 5

Sequence	Wage	Motif	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AA	strain	Mol.							
DPPQSPGQA	9	3	60	P2A					
APATTEQQTA	10	2	30	P2A					
FPDLSSEFOA	10	2/3	98	P2A					
APATTEQQAA	10	3	30	P2A					
DPIGHLYIPIA	10	3	170	P2A					
EADPTQHSY	9	1	161	1	0.56	0	0	0.0002	<0.0002
KVADLWQPL	10	1	105		0.0005	0.041	0.0039	0.0030	0.0070
ASSLPTTINX	10	3	8	1	2.3			0.043	
TQDLVQKX	9	1	240	1	0.57	0.0001	0	0	0
LVQDKYLEY	9	1	243	3	016	0	0.0016	0.0098	0
ILIMQPIV	9	3			<0.0007	1.4	0.0048	0.0048	0
EVDPICHY	9	3			3.7			0.0022	
ASSPSTTINY	10	2	8	1	0.016	0	0.0016	0.0054	0
VTCLGQSY	8	1	172	1	0.022	0	0.0001	0.0007	0
ESSLPTTINY	9	3	9	1	0.037	0	0.013	0.12	0
GSVVGKQY	9	3	77	1	0.0059	0	0.0009	0.025	0
DVQDKYLEY	10	1	new	242	3	0	0.0010	0	0
SSSPSTTINY	9	2	9	1	0.016	0	0.0095	0.056	0
MLESVINKY	9	1	128	1	0.0016	0.0002	0.0006	0	0
KMVELVHPL	9	2			<0.0007	0.13	0.0007	0	0.0043
KKVELVHPL	10	2	105		<0.0008	0.071	0.0004	0.0001	0.0008
LVQDKYLEY	10	3			0.0030	0.065	0.0007	0	0

Table 5

Sequence	AA	Mass strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
SLPRAVAVRK	9	1		96	3,11	<0.0007	0.0001	3.9	2.6	0
ADLVGFLLK	10	1		107	3	0.0012	0.0003	0.0081	0.022	0
ZSLPRAVAVRK	10	1		95	3	<0.0008	0	0.0090	0.0052	0
MLESVIKINYK	10	1				0	0	0.034	0.0045	0
LVGFLLK	8	1		109	3	0.0029	0.0002	0.027	0.034	0
TTINFRTRQR	9	1		66	3,11	0	0	0.051	0.40	0
LLGDNQIMPK	10	1/3		182	3,11	<0.0007	0.0001	0.022	0.016	0
SIVMEYDGR	9	-	1	219	3,11	<0.0006	0	0.059	0.32	0
HSAYGEPRK	9	1		229	3	0.0007	0	0.0070	0.0015	0
LLTQDLVQEK	10	1		238	3,11	<0.0007	0	0.0014	0.011	0
LTDQDLVQEK	9	1		239	3,11	0.0011	0	0.0002	0.16	0
NYKHCPEPEIT	10	1		135	24	0	0	0	0	0.26
LYIPATCQL	10	3		115	24	<0.0007	0	0.0006	0	0.0035
NYPLWSQSY	9	3		16	24	<0.0006	0	0	0.0001	0.016
SYVVLVCL	8	1		168	24	0.0029	0.00025	0.0020	0.0002	0.0026
ETSIVVLEI	10	1				0.075	0	0.0009	0.0004	0
TSYVKVLEY	9	1		275	3	0.082	0	0.23	0.013	0
FLWGPRLA	9	1				<0.0006	0.027	0.0015	0	0
ALAEETSYKV	10	1		271		<0.0007	0.017	0.0011	0.0029	0
RVRRPPPSLR	10	1		290	3	<0.0007	0	0.25	0.0035	0
ALAEETSYK	9	1				<0.0006	0.0002	0.17	0.39	0
LTDQDLVQEYK	10	1		239	1	0.041	0	0	0.0002	0

Table 5

Sequence	AA	Residue String	Vol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GFLLLKYRA	9	1							0.0004	0.0002
CPPREIFGKA	9	1					0	0	0	0
FFFFPSLREAA	9	1					0	0	0	0
PPPSLREAA	9	1					0	0	0	0
HCPPPEIPGK	9	1		138	3,11				0.0017	0.00022
RSLHICPPEEA	10	1							0.0001	0.0008
EPLHGGPRLA	10	1					0	0	0	0
RPPPPSPLREAA	10	1						0.0004	0	0
PPPPSPLREAA	10	1					0	0	0	0

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max.
					Binding						
FSPAFDNLY	c-ErhB2			1213	A01	5.5000	0.0010				5.5000
CMQIAKGMSY	c-ErhB2			826	A01	0.2967	0.0003				0.2967
ESMPNPEGRY	c-ErhB2			280	A01	0.1800	0.0003				0.1800
ASCVTACPY	c-ErhB2			293	A01	0.0552	0.0008				0.0552
FSPAFDNLY	c-ErhB2			1213	A01	0.0425	0.0002				0.0425
ASPLDSTFY	c-ErhB2			997	A01	0.0290	0.0002				0.0290
RGTOLFEDNY	c-ErhB2			101	A01	0.0205	0.0003				0.0205
PASPLDSTFY	c-ErhB2			996	A01	0.0148	0.0003				0.0148
L.SAFSLHSY	ICV			2889	A01	0.8100	0.0002				0.8100
KSTKVPAAY	ICV			1216	A01	0.0134	0.0009				0.0134
DSSVLCECY	ICV			1513	A01	0.0110	0.0002				0.0110
ETDPIGHLY	MAGE-Ju	3	analog	161	A01	12.5000					12.5000
AVDPIGHLY	MAGE-3a	3	analog	161	A01	8.0000					8.0000
EVDPIGHLY	MAGE-Ju	3	analog	161	A01	5.5000					5.5000
EVDAIGHLY	MAGE-Ju	3	analog	161	A01	5.3500					5.3500
EVDPIGHLY	MAGE-3a	3	analog	161	A01	5.0000					5.0000
EVDPIGHAY	MAGE-Ju	3	analog	161	A01	4.6500					4.6500
EADPIGHLY	MAGE-Ju	3	analog	161	A01	3.4500					3.4500
EVDPTGHLY	MAGE-3a	3	analog	161	A01	2.9500					2.9500
EVDPIGHISY	MAGE-Ju	3	analog	161	A01	2.6667					2.6667
EVDPAIGHLY	MAGE-Ju	3	analog	161	A01	2.4000					2.4000
EVDPIGHILA	MAGE-3a	3	analog	161	A01	0.3300					0.3300
EVAPIGHLY	MAGE-Ju	3	analog	161	A01	0.1800					0.1800
EVDPASNTY	MAGE-4	4		161	A01	1.5000					1.5000
VGSDCTTHY	P53			225	A01	0.2600	0.0003				0.2600
PSQKTYQGSY	P53			98	A01	0.0140	0.0003				0.0140
PLSEDQDOLY	PAP			147	A01	1.2000	0.0005				1.2000
IPSYKIMY	PAP			277	A01	0.5650	0.0001				0.5650
YASCHLTEL	PAP			310	A01	0.5467	0.0003				0.5467

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max. Binding
RVLQGLIPREY	c-ERB2			545	A03	0.0015	0.00350	0.00150	0.0012	0.00350	0.00112
OIVTQIIMPY	c-ERB2			795	A03	0.0024	0.0112	0.0039	0.0079	0.0012	0.00575
VMAGVGSPY	c-ErbB2			771	A03	0.0400	0.0575	0.0016	0.2667	0.00440	0.2667
ILWKAGILY	IBV	adr	POL	724	A03	0.0017	0.2667	0.0016	0.0016	0.0016	0.0016
ILRGTSFVY	IIIV	adr	POL	145	A03	0.0017	0.0440	0.0002	0.1160	0.00103	0.00103
KLNWASQIY	IIIV	adr	POL	958	A03	0.0070	0.1160	0.0006	0.0006	0.0006	0.0006
CLNKIVRMY	MAGE-1		GAG	274	A03	0.0017	0.0003	0.0002	0.0002	0.0002	0.0002
IYGFLLKY	MAGE-1			109	A03	0.0033	0.0563	0.0012	0.0012	0.0012	0.00563
GTRVRAIAV	PS3			154	A03	0.0027	0.0365	0.0002	0.0002	0.0002	0.00165
KJQNFRRVYY	IIIV		POL	1474	A03/A11	0.0056	0.1190	0.1350	0.1350	0.1350	0.1350
SLYTKVVHY	PSA			217	A03/A11	0.0017	0.6750	0.0140	0.0140	0.0140	0.6750
LTCGPADIMGY	HCV			126	A11	2.4500	0.0003	0.0120	0.0001	0.0001	2.4500
ETAYFULK	IIIV	con		1351	A11		0.0037	0.0425	0.0425	0.0425	0.0425
RWGLLLALL	c-ErbB2			8	A24				1.2567	1.2567	
PYVSRLLLGI	c-ErbB2			780	A24				0.1650	0.1650	
VYMIMVKCW	c-ErbB2			951	A24				0.1640	0.1640	
AYSITLQCL	c-ErbB2			440	A24				0.1250	0.1250	
SYGVTWEL	c-ErbB2			907	A24				0.1200	0.1200	
IYISAWPDSL	c-ErbB2			410	A24				0.0835	0.0835	
WWSYGVTVW	c-ErbB2			905	A24				0.0800	0.0800	
SYGVTWELM	c-ErbB2			907	A24				0.0630	0.0630	
TYIPTNASL	c-ErbB2			63	A24				0.0375	0.0375	
VYMIMVKCW	c-ErbB2			951	A24				0.0218	0.0218	
RFRELVSEF	c-ErbB2			968	A24				0.0180	0.0180	
CYGLGMEHL	c-ErbB2			342	A24				0.0176	0.0176	
KWMALESIL	c-ErbB2			887	A24				0.0149	0.0149	
EYLVPQQGFF	c-ErbB2			1022	A24				0.0120	0.0120	
RYSEDDPTVPL	c-ErbB2			1111	A24				0.0117	0.0117	
RFTHQSDDW	c-ErbB2			898	A24				0.0107	0.0107	

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max. Binding
EYLVSFGVWI	IBV		NUC	117	A24				0.0335		
WFIISCLTF	IBV		NUC	102	A24				0.0300	0.0300	
OYLAGLSTI	ICV			177	A24				0.0475	0.0475	
TYSTYIGKFL	ICV			1296	A24				0.0225	0.0225	
OYSPGQRVEF	ICV			2614	A24				0.0175	0.0175	
KFMLCAGRW	PSA			190	0.0003				0.0305	0.0305	

Table 6

AA	SEQUENCE	SOURCE
9	GLNKIVRMY	HIV GAG 274
9	KLNWASQIY	HIV POL 958
9	KIQNFRVYY	HIV POL 1474
9	TLWKAGILY	HBV adr POL 724
9	ILRGTSFVY	HBV adr POL 1345
9	SLYTKVVHY	PSA 237
9	NTSSSPQPK	p53 311
9	NVKIPVAIK	c-ERB2 745
10	TLGFGAYMSK	HCV LORF 1261
10	GTRVRAMAIY	p53 154
10	EAYSPVSTSK	HBV adw POL 887
9	QITKIQNFR	HIV POL 1471
9	NITGLILTR	HIV ENV 2633
9	FLWEWASVR	HBV adr ENV 324
9	RTPSPRRRR	HBV adr CORE 549
9	SLARGNQGR	HBV adr POL 805
10	VAYQATVCAR	HCV LORF 1587
10	KTYQGSYGFR	p53 101
9	WMCLRRFII	HBV ayw 237
9	WMCLRRFII	HBV ayw 237-245
9	KFMLCAGRW	PSA 190
10	IMPKTGFLII	MAGE 1 188
8	ETAYFLLK	HIV con 1351
11	LTCCGFADIMGY	HCV 126
9	CSPHHTALR	HBV NUC,XNUCFUS 48
9	VMPKTGLLI	MAGE 2 188
9	VMPKTGLLI	MAGE2 188-196
9	VAELVHFLL	MAGE 3 106
9	IMPKAGLLI	MAGE 3 188
10	VMPKTGLLI	MAGE 2 188
10	VMPKTGLLI	MAGE2 188-197

AA	SEQUENCE	SOURCE
9	ASCVTACPY	c-ErbB2 293
9	VMAGVGSPY	c-ErbB2 773
9	ASPLDSTFY	c-ErbB2 997
9	FSPAfdnLY	c-ErbB2 1213
9	KSTKVPAAY	HCV 1236
9	DSSVLCECY	HCV 1513
9	LSAFSLHSY	HCV 2889
9	PLSEDQLLY	PAP 147
9	YAVCDKCLK	HPV 16 E6 67
9	CMSCCRSSR	HPV 16 E6 143
9	RWGLLLALL	c-ErbB2 8
9	TYLPTNASL	c-ErbB2 63
9	CYGLGMEHL	c-ErbB2 342
9	AYSLTLQGL	c-ErbB2 440
9	PYVSRLLGI	c-ErbB2 780
9	KWMALESIL	c-ErbB2 887
9	RFTHQSDVW	c-ErbB2 898
9	VWSYGVTWW	c-ErbB2 905
9	SYGVTWEL	c-ErbB2 907
9	VYMIMVKCW	c-ErbB2 951
9	RFRELVSEF	c-ErbB2 968
9	WFHISCLTF	HBV NUC 102
9	TYSTYGKFL	HCV 1296
9	QYLAGLSTL	HCV 1777
10	IPSYKKLIMY	PAP 277
10	RGTQLFEDNY	c-ErbB2 103
10	ESMPNPEGRY	c-ErbB2 280
10	CMQIAKGMSY	c-ErbB2 826
10	PASPLDSTFY	c-ErbB2 996
10	FSPAfdnLYY	c-ErbB2 1213
10	PSQKTYQGSY	p53 98
10	VGSDCTTIHY	p53 225
10	YASCHLTEL	PAP 310
10	LYISAWPDSL	c-ErbB2 410

AA	SEQUENCE	SOURCE
10	SYGVTVWELM	c-ErbB2 907
10	VYIMIMVKCWM	c-ErbB2 951
10	EYLVPQQGFF	c-ErbB2 1022
10	RYSEDPTVPL	c-ErbB2 1111
10	EYLVSGFGVWI	HBV NUC 117
10	QYSPGQRVEF	HCV 2614
9	VYNFATCGI	LCMV glyco 35
9	GYCLTKWMI	LCMV glyco 283
9	MFEALPHII	LCMV glyco 7
9	IFALISFLL	LCMV glyco 43
9	LFKTTVNSL	LCMV glyco 342
9	LYTVKYPNL	LCMV nucleo 204
9	PYIACRTSI	LCMV nucleo 314
10	GYCLTKWMIL	LCMV glyco 283
10	AYLVSIFLHL	LCMV glyco 446
9	RWCIPWQRL	CEA 10
9	IYPNASLLI	CEA 101
9	LWWVNNQSL	CEA 177
9	LYGPDAPTI	CEA 234
9	VYAEPPKPF	CEA 318
9	LWWVNNQSL	CEA 355
9	LYGPDDPTI	CEA 412
9	TYYRPGVNL	CEA 425
9	LYGPDTPII	CEA 590
9	QYSWRINGI	CEA 624
9	TYACFVSNL	CEA 652
9	VWKTWGQYW	gp100 152
9	TWGQYWQFL	gp100 155
9	RYGSFSVTL	gp100 479
9	LMAVVLASL	gp100 606
9	HWLRLPRIF	gp100 636
9	SYKHEQVYI	PAP 96
9	AMTNLAALF	PAP 116
9	VFLTLSVTW	PSA 2

AA	SEQUENCE	SOURCE
9	TWIGAAPLI	PSA 9
9	CYASGWGSI	PSA 148
10	YMIMVKCWMI	c-ErbB2 952
10	RWCIPWQRLL	CEA 10
10	FWNPPTTAKL	CEA 27
10	QYSWFVNNTF	CEA 268
10	TFQQSTQELF	CEA 276
10	VYAEPPKPFI	CEA 318
10	YYRPGVNLSL	CEA 426
10	QYSWLIIDGNI	CEA 446
10	SYLSGANLNL	CEA 604
10	HFLRNQPLTF	gp100 231
10	LFPPEGVSIW	PAP 123
10	TWIGAAPLIL	PSA 9
10	HYRKWIKDTI	PSA 244
9	KLRKPKHKK	<i>P. falciparum</i> CSP 104
9	KILSVFFLA	<i>P. falciparum</i> EXP-1 2
9	ALFFIIFNK	<i>P. falciparum</i> EXP-1 10
9	GTGSGVSSK	<i>P. falciparum</i> EXP-1 28
9	VLYNTEKGR	<i>P. falciparum</i> EXP-1 99
9	KYKLATSVL	<i>P. falciparum</i> EXP-1 73
9	PSENERGYY	<i>P. falciparum</i> LSA1 1664
9	FLKENKLNK	<i>P. falciparum</i> LSA1 111
9	GVSENIFLK	<i>P. falciparum</i> LSA1 105
9	ILVNLLIFH	<i>P. falciparum</i> LSA1 12
9	KSLYDEHIK	<i>P. falciparum</i> LSA1 1854

AA	SEQUENCE	SOURCE
9	LLIFHINGK	P. falciparum LSA1 16
9	QSSLQPQDNR	P. falciparum LSA1 1676
9	QTNFKSLLR	P. falciparum LSA1 94
9	RINEEKHEK	P. falciparum LSA1 49
9	SLYDEHIKK	P. falciparum LSA1 1855
9	VLAEDLYGR	P. falciparum LSA1 1647
9	VLSHNSYEK	P. falciparum LSA1 60
9	FYFILVNLL	P. falciparum LSA1 9
9	YYIPHQSSL	P. falciparum LSA1 1671
9	PSDGKCNLY	P. falciparum TRAP 207
9	LACAGLAYK	P. falciparum TRAP 511
9	LLACAGLAY	P. falciparum TRAP 510
9	LSTNLPYGR	P. falciparum TRAP 122
9	QGINVAFNR	P. falciparum TRAP 192
9	RGDNFAVEK	P. falciparum TRAP 307
9	RSRKREILH	P. falciparum TRAP 262
9	SLLSTNLPY	P. falciparum TRAP 120
9	KYLVIVFLI	P. falciparum TRAP 8
9	PYAGEPAPF	P. falciparum TRAP 528

AA	SEQUENCE	SOURCE
10	VTCGNGIQVR	<i>P. falciparum</i> CSP 375
10	GTGSGVSSKK	<i>P. falciparum</i> EXP-1 28
10	LALFFIIFNK	<i>P. falciparum</i> EXP-1 9
10	FQDEENIGIY	<i>P. falciparum</i> LSA1 1794
10	FILVNLLIFH	<i>P. falciparum</i> LSA1 11
10	HVLSHNSYEK	<i>P. falciparum</i> LSA1 59
10	KSLYDEHIKK	<i>P. falciparum</i> LSA1 1854
10	ALLACAGLAY	<i>P. falciparum</i> TRAP 509
10	IIRLHSDASK	<i>P. falciparum</i> TRAP 100
10	LLACAGLAYK	<i>P. falciparum</i> TRAP 510
10	RLHSDASKNK	<i>P. falciparum</i> TRAP 102
9	ILGFVFVFTL-NH2	Flu Matrix 59-67
10	KGILGFVFVTL- NH2	Flu Matrix 57-66
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
11	KQVPLRPMTYK	940.03 N-terminal extension
9	KLYEIVAKV	A2.1 consensus
9	KLAEYVAKV	A2.1 consensus
9	KLAEIVYKV	A2.1 consensus
9	KVFEYLINK	A3.2 consensus
10	KVFPYALINK	A3.2 consensus
9	AVFAYAAAK	A3.2 consensus
9	ALEPAIAKY	A1 consensus

AA	SEQUENCE	SOURCE
9	YLEPAIAKY	A1 consensus
9	ALEPYIAKY	A1 consensus
9	YLEQYIEKY	A1 consensus
9	GTEKLLAKY	A1 consensus
9	ATEPAIAKY	A1 consensus
9	ATNYPAIQK	A11 consensus
9	ATNVPAIQK	A11 consensus
9	ATNAPYIQK	A11 consensus
9	ATNAVYIQK	A11 consensus
9	ATNAAYAQK	A11 consensus
9	AVNAAYAQK	A11 consensus
9	AVNAPYIQK	A11 consensus
9	AVNAVYIQK	A11 consensus
9	PTDPKLINY	A1 consensus
9	GTDPKLINY	A1 consensus
9	YTDPKLINF	A1 consensus
9	FTDPKLINY	A1 consensus
9	FTDQAVIKY	A1 consensus
9	YTDQAVIKF	A1 consensus
9	YTDQKLNINF	A1 consensus
9	STNPKPQKK	HCV-core 2-10
11	STNPKPQKKNK	HCV-core 2-12
9	SFFPEITYI	self peptide of P815 analog: Y2 to F.
9	ATDPNFLY	A1 consensus
9	ATDKNFLY	A1 consensus
9	ALMEKIYQV	A2.1 consensus peptide
9	ALSEKIYQV	A2.1 consensus peptide
9	AVYDPIIQK	A3.2 consensus peptide
9	AVYDKIIQK	A3.2 consensus peptide
9	AVMNPMIQK	A11 consensus peptide

AA	SEQUENCE	SOURCE
9	AVMNEMIQK	A11 consensus peptide
9	AYMDMVNSF	A24 consensus peptide
9	AYIDNVNSF	A24 consensus peptide
9	KLAAAAAAK	A3.2/A11 poly-A analog
9	DVFRDPALK	Aw68 endogenous
9	GYKDGEYI	Lm listeriolysin 91-99
10	MMWYWGPSLY	HBV
11	WMMWYWGPSLY	HBV
9	RYLRDQQLL	HIV env
8	FLLLKRYRA	MAGE-1
9	IMPKTGFLI	MAGE-1
9	VADLVGFLL	MAGE-1
10	IMPKTGFLII	MAGE-1
11	FLIIVLVMIAM	MAGE-1
11	CILESCFRAVI	MAGE-1
9	MYRPDAIQL	P. Yoelii SSP2 143
10	NYSPNGNTNL	P. Yoelii SSP2 119
9	KFNPMKTHI	Kd consensus peptide
9	AMIKNLDFI	Db consensus
9	AMIKNLYFI	Db consensus analog
11	STLPETYYVRR	HCV 141-151 analog
9	QYDDAVYKL	Cw4 consensus
10	FQDPQERPRK	HPV16 E6
10	VFEFAFKDLF	HPV18 E6
9	VVYRDSIPH	HPV18 E6
9	IFEANGNLI	Flu HA 240-248
9	IYATVAGSL	HA 529-537

AA	SEQUENCE	SOURCE
9	SYIPSAEKI	P. bergaii CS 252-260
9	KYQAVITTL	Tumour P198 14-22
10	MYPHFMPTNL	MCMV pp89 167-176
9	AYPNVSAKI	Lm listeriolysin 196-204
9	AYTGGKIN	Lm listeriolysin 413-421
9	SAISSILSK	HBV ENV 159
9	QAGFFLLTK	HBV ENV 190
9	SALYREALK	HBV NUC 64
9	RAKWNNTLK	HIV env 370
9	RATQIPSYK	PAP 273
9	TAAHCIRNK	PSA 58
9	MAVFIHNFK	HIV pol 909
9	TAGILELLK	HPV 6b E1 192
9	RAALLGKFK	HPV 6b E1 205
9	CATMCRHYK	HPV 6b E1 406
9	TAACSHEGK	Flu HA-1 132
9	NANANSAVK	P. fal csp 304
9	GAFKVPGVK	LCMV glyco 484
9	RARVHPTTR	HBV POL 244
9	CALPFTSAR	HBV X 69
9	NMLESILIK	LCMV mac 259
9	WMILAAELK	LCMV glyco 289
9	EMNLPGRWK	HIV pol 107
9	SSLQSKHRK	HBV POL 201
9	GSTHVSWPK	HBV POL 398
9	TSDLEAYFK	HBV X NUC FUS 105
9	ASQIYAGIK	HIV pol 438
9	ASCDKCQLK	HIV pol 769
9	MSLAADLEK	LCMV mac 100
9	VSSKNLMEK	Met. tyro 25

AA	SEQUENCE	SOURCE
9	LSTNL PYGK	P. fal ssp2 122
9	STDHIPILY	A1 Nat. Processed
9	STAPPAHGV	Breast mucin 9-17
9	LMAVVVLASL	gp100
9	WSQKRSFVY	gp100
9	PLDCVLYRY	gp100
10	PSSVGSRSEY	gp100
9	YTAVVPLVY	Hu J chain 102-110

Table 7

AA	SEQUENCE	SOURCE
8	LTELTYFEK	PAP 315
9	TISPSYTYY	CEA 419
9	GTGCNGWFY	HPV 16/18 E1 11
9	LTEMVQWAY	HPV 6b/11 E1 358
9	ITVNNNSGSY	CEA 289
9	CTGWFMFVVA	HPV 6b/11 E1 14
9	ATVQDLKRK	HPV 6b/11 E1 77
9	AVESEISPR	HPV 6b/11 E1 101
9	FLNSNMQAK	HPV 6b/11 E1 393
9	ITRQTVIEH	HPV 6b/11 E1 341
9	IVGPPDTGK	HPV 6b/11 E1 476
9	KLIEPLSLY	HPV 6b/11 E1 254
9	KLWLHGTPK	HPV 6b/11 E1 462
9	KMSIKQWIK	HPV 6b/11 E1 420
9	VVAGFGIHH	HPV 6b/11 E1 238
9	HLFGYSWYK	CEA 61
9	ISPSYTYYR	CEA 420
9	HTQVLFIAK	CEA 636
9	ITVYAEPPK	CEA 316
9	ITVSAELPK	CEA 494
9	RLQLSNGNR	CEA 190
9	RLQLSNGNR	CEA 546
9	RINGIPQQH	CEA 628
9	SNMQAKYVK	HPV 6b/11 E1 396
9	EWITRQTVI	HPV 6b/11 E1 339
9	FFERLSSSL	HPV 6b/11 E1 613
9	NWKPTVQFL	HPV 6b/11 E1 439
10	PTISPSYTYY	CEA 418
10	PTISPLNTSY	CEA 240
10	HSASNPSPQY	CEA 616
10	KLIEPLSLYA	HPV 6b/11 E1 254
10	AVGPPDTGK	HPV 6b/11 E1 475
10	DCATMCRHYK	HPV 6b/16 E1 405
10	KLWLHGTPKK	HPV 6b/11 E1 462
10	WVAGFGIHH	HPV 6b/11 E1 237

AA	SEQUENCE	SOURCE
10	TITVSAELPK	CEA 493
10	TFWNPPPTAK	CEA 26
10	TISPSYTYYR	CEA 419
10	TISPLNTSYR	CEA 241
10	RTLTLFNVTR	CEA 198
10	RTLTLFNVTR	CEA 554
10	RTLTLLSVTR	CEA 376
10	ATPGPAYSGR	CEA 89
10	ASGHSRTTVK	CEA 483
10	QFLRHQNIEF	HPV 6b/11 E1 445
10	TFTFPNPFPPF	HPV 6b/11 E1 586
9	RVDCTPLMY	Prost.Ca PSM 463
9	LLSLYGIHK	Prost.Ca PAP 243
9	SIVLPFDRCR	Prost.Ca PSM 590
9	KSLYESWTK	Prost.Ca PSM 491
9	SMKHPQEMK	Prost.Ca PSM 615
9	SLYESWTKK	Prost.Ca PSM 492
9	YSLVHNLT	Prost.Ca PSM 471
9	HLTELYFEK	Prost.Ca PAP 314
9	RATQIPSYK	Prost.Ca PAP 273
9	ASGRARYTK	Prost.Ca PSM 531
9	SLYGIHKQK	Prost.Ca PAP 245
9	RDYAVVLRK	Prost.Ca PSM 598
9	SSHDLMLLR	Prost.Ca PSA 113
9	GAAPLILSR	Prost.Ca PSA 12
9	KIVIARYGK	Prost.Ca PSM 199
9	RAAPILLAR	Prost.Ca PAP 2
9	VVLRKYADK	Prost.Ca PSM 602
9	GLPDRPFYR	Prost.Ca PSM 680
9	WLDRSVLAK	Prost.Ca PAP 25
9	KVFRGNVK	Prost.Ca PSM 207
9	IVRSFGTLK	Prost.Ca PSM 398
9	KIYSISMKH	Prost.Ca PSM 610
9	RSVLAKELK	Prost.Ca PAP 28
9	STNEVTRIY	Prost.Ca PSM 348
9	GFFLLGFLF	Prost.Ca PSM 31

AA	SEQUENCE	SOURCE
9	LYSDPADYF	Prost.Ca PSM 227
9	KYADKIYSI	Prost.Ca PSM 606
9	NYARTEDFF	Prost.Ca PSM 178
9	AYINADSSI	Prost.Ca PSM 448
5	SASF CGSPY	HBV POL 165
9	AFTFSPTYK	HBV POL 655
9	SVVRRAPPH	HBV POL 524
9	RWMCLRRFI	HBV ENV 236
10	SWLSLLVPP	HBV ENV 334
9	SWWTSLNFL	HBV ENV 197
9	PWTHKVGNF	HBV POL 51
9	SFCGSPYSW	HBV POL 167
10	NADSSIEGNY	Prost.Ca PSM 451
10	GLDSVELAHY	Prost.Ca PSM 104
15	RATQIPSYKK	Prost.Ca PAP 273
10	LGFLFGWFIK	Prost.Ca PSM 35
10	SSIEGNYTLR	Prost.Ca PSM 454
10	KSLYESWTKK	Prost.Ca PSM 491
10	SLLSLYGIHK	Prost.Ca PAP 242
20	FLYNFTQIPH	Prost.Ca PSM 73
10	VIYAPSSHNK	Prost.Ca PSM 690
10	AVVLRKYADK	Prost.Ca PSM 601
10	KSPDEGFEGK	Prost.Ca PSM 482
10	IVRSFGLTLLK	Prost.Ca PSM 398
25	RIYNVIGTLR	Prost.Ca PSM 354
10	LSLYGIHKQK	Prost.Ca PAP 244
10	MSLLKNRFLR	Prost.Ca PSA 99
10	ISMKHPQEMK	Prost.Ca PSM 614
10	RAVCGGVLVH	Prost.Ca PSA 43
30	GSAPPDSSWR	Prost.Ca PSM 311
10	SIPVHPIGYY	Prost.Ca PSM 291
10	CSGKIVIARY	Prost.Ca PSM 196
10	ETYELVEKFY	Prost.Ca PSM 557
10	RLLQERGVAY	Prost.Ca PSM 440
35	FYDPMFKYHL	Prost.Ca PSM 565
10	TYSVSFDSLF	Prost.Ca PSM 624

5

10

15

20

25

30

35

AA	SEQUENCE	SOURCE
10	LYNFTQIPHL	Prost.Ca PSM 74
10	GWRPRRTILF	Prost.Ca PSM 409
10	FAAPFTQCGY	HBV POL 631
10	RWMCLRRFII	HBV ENV 236
10	WFVGLSPTVW	HBV ENV 345
10	SWPKFAVPNL	HBV POL 392
10	VFADATPTGW	HBV POL 686
9	FIFHKFQTK	HTLV-I tax 276
9	FLTNVPYKR	HTLV-I tax 182
9	ITWDPIDGR	HTLV-I tax 54
9	SALQFLIPR	HTLV-I tax 66
9	LSFPDPGLR	HTLV-I tax 131
9	QSSSFIFHK	HTLV-I tax 272
9	GLCSARLHR	HTLV-I tax 34
9	RLPSFPTQR	HTLV-I tax 74
9	AMRKYSPFR	HTLV-I tax 108
9	ISGGLCSAR	HTLV-I tax 31
9	ALFTAQEAK	HPV 16 E1 69
9	ATMCRHYKR	HPV 16 E1 406
9	FMSFLTALK	HPV 16 E1 453
9	GVSFSELVR	HPV 16 E1 216
9	KAAMLAFK	HPV 16 E1 204
9	LTNILNVLK	HPV 16 E1 191
9	LVRPFKSNK	HPV 16 E1 222
9	MSFLTALKR	HPV 16 E1 454
9	NSNASAFLK	HPV 16 E1 386
9	QMSMSQWIK	HPV 16 E1 419
9	RLKAICIEK	HPV 16 E1 109
9	SLFGMSLMK	HPV 16 E1 484
9	SMSQWIKYR	HPV 16 E1 421
9	TAAALYWYK	HPV 16 E1 315
9	VVLLLVRYK	HPV 16 E1 274
9	ALLRYKCGK	HPV 18 E1 284
9	ATMCKHYRR	HPV 18 E1 413
9	CATMCKHYR	HPV 18 E1 412
9	FITFLGALK	HPV 18 E1 460

AA	SEQUENCE	SOURCE
9	GVLILALLR	HPV 18 E1 279
9	KLRAGQNHR	HPV 18 E1 647
9	LILALLRYK	HPV 18 E1 281
9	LTTNIHPAK	HPV 18 E1 571
5	NMSQWIRFR	HPV 18 E1 428
9	NSNAAAFLK	HPV 18 E1 393
9	SVAALYWYR	HPV 18 E1 322
9	WTYFDTYMR	HPV 18 E1 536
9	YVQAIVDKK	HPV 18 E1 19
10	IIKNFDIPK	GCDFP-15 36
9	VLA VQTELK	GCDFP-15 55
10	IIKNFDIPK	GCDFP-15 35
10	TACLCDDNPK	GCDFP-15 87
10	AVLA VQTELK	GCDFP-15 54
15	TFYWDFTYTR	GCDFP-15 97
9	ASCHLTELY	PAP 311
10	KGEYFVEMYY	PAP 322
10	LTAAHCIRNK	PSA 57
9	PLYDMSLLK	PSA 95
20	QVHPQKVTK	PSA 182
9	SLLKNRFLR	PSA 100
9	YTKVVHYRK	PSA 239
9	TLWKAGILY	HBV pol 150
9	SLYTKVVHY	PSA 237
25	PVNRPIDWK	HBV POL 612
9	RHYLHTLWK	HBV POL 719
11	HTLWKAGILYK	HBV POL 149
11	GTDNSVVLRSK	HBV POL 735
11	RVTGGVFLVDK	HBV POL 357
30	ATQIPSYK	PAP 274
9	WMNSTGFTK	HCV consensus
9	RVLEDGVNY	HCV consensus
9	RLLAPITAY	HCV consensus
9	GVLAALAAAY	HCV consensus
35	RVCEKMLAY	HCV consensus

TABLE 8

PEPTIDE	AA	SEQUENCE
1235.01	10	AVFDRKSDAK
26.0149	9	CALRFTSAR
26.0153	9	SSAGPCALR
F104.02	9	SLTPPHSAK
F105.01	9	AIFQSSMTK
F105.02	9	GIFQSSMTK
F105.03	9	AAFQSSMTK
F105.04	9	AIAQSSMTK
F105.05	9	AIFASSMTK
F105.06	9	AIFQASMTK
F105.07	9	AIFQSAMTK
F105.08	9	AIFQSSATK
F105.09	9	AIFQSSMAK
F105.10	9	AIFQSSMTA
F105.11	9	FIFQSSMTK
F105.12	9	SIFQSSMTK
F105.14	9	ANFQSSMTK
F105.16	9	AIFQCSMTK
F105.17	9	AIFQSSMTR
F105.19	9	AIFQSSMTY
F105.20	9	AILQSSMTR
F105.21	9	AIFQRSMTR
F105.24	10	PAIFQSSMTK
F105.25	10	AIFQSSMTKJ
27.0103	9	AIIIHQQQK
27.0104	9	YGFRILGFLH
27.0108	9	SSCMGGMNR
27.0235	10	TCTYSPALNK
27.0239	10	NSSCMGGMNR
27.0240	10	SSCMGGMNRR
27.0250	10	KSKKGQTSR
27.0252	10	TSRHKKLMFK
28.0062	8	FMFSPTYK
28.0063	8	FVFSPTYK
28.0066	8	TMLXMXKK

5

10

15

20

25

30

35

PEPTIDE	AA	SEQUENCE
28.0322	9	SMICSVVRR
28.0323	9	SVICSVVRR
28.0324	9	KVGNFTGLK
28.0325	9	KVGNFTGLR
28.0326	9	VVFFSQFSR
28.0327	9	SVNRPIDWK
28.0328	9	TLWKAGILK
28.0329	9	TLWKAGILR
28.0330	9	TMWKAGILY
28.0331	9	TVWKAGILY
28.0332	9	RMYLHTLWK
28.0333	9	RVYLHTLWK
28.0334	9	AMTFSPTYK
28.0335	9	AVTFSPTYK
28.0336	9	SVVRRAFPR
28.0337	9	SVVRRAFPK
28.0338	9	ISEYRHYXY
28.0339	9	GTGXNGWFY
28.0340	9	ASXHILTELY
28.0341	9	ASXDKXQLK
28.0371	9	RVXEKMALY
28.0372	9	XTGWFPMVEA
28.0374	9	HISXLTPGR
28.0375	9	AVXTRGVAK
28.0377	9	HLIFXHSKK
28.0378	9	HTMLXMXKK
28.0381	9	RLKADKIEK
28.0383	9	TLFXASDAK
28.0384	9	ALLRYKXGK
28.0387	9	ATMXRHYKR
28.0388	9	XATMXRHYK
28.0390	9	ATMXKHYRR
28.0391	9	LLAXAGLAY
28.0392	9	LAXAGLAYK
28.0393	9	STVLPFDXR
28.0394	9	AAXWWAGIK
28.0628	10	QMFTEFSPTYK

PEPTIDE	AA	SEQUENCE
28.0629	10	QVFTPSPTYK
28.0630	10	TMWKAGILYK
28.0631	10	TVWKAGILYK
28.0632	10	VMGGVFLVDK
28.0633	10	VVGGVFLVDK
28.0635	10	SVLPETTVVR
28.0638	10	HTLWKAGILK
28.0640	10	HMLWKAGILY
28.0395	9	SAIXSVVRR
28.0644	10	GTFNSVVLSR
28.0645	10	YMFDVVLGAK
28.0646	10	MMWYWGPSLK
28.0647	10	MMWYWGPSLR
28.0665	10	IVGGWEXEK
28.0667	10	IIIEXVYXK
28.0668	10	SIPHAAXHK
28.0670	10	IVXPIXSQK
28.0671	10	LIRXLRXQK
28.0672	10	XTYSPALNK
28.0675	10	TVXAGGXAR
28.0676	10	HISXLTPGR
28.0677	10	XVNXSQFLR
28.0678	10	LIFXHSKKK
28.0679	10	FVLGGXRHK
28.0713	10	TSADKSVVRR
28.0714	10	HLIFXHSKKK
28.0715	10	LLIRXINXQK
28.0716	10	GIVXPIXSQK
28.0717	10	LLIRXLRXQK
28.0718	10	SLEQRSLHYK
28.0720	10	RIVGGWEXEK
28.0721	10	DIILEXVYXK
28.0722	10	XVYXKQQLLR
28.0723	10	RAVXGGVLVH
28.0725	10	LTAAHXIRNK
28.0728	10	KAAXWWAGIK
28.0730	10	VVRRXPHHER

5

10

15

20

25

30

35

PEPTIDE	AA	SEQUENCE
28.0731	10	LLGIWGXS ^G K
28.0732	10	TTLFXASDAK
28.0734	10	RTVXAGGXAR
28.0736	10	GTQRXEKXSK
28.0737	10	LVQ NANPDXK
28.0738	10	VTXGNGIQVR
28.0739	10	DXATMXRHYK
28.0740	10	GLAXHQLXAR
28.0741	10	ALLAXAGLAY
28.0742	10	LLAXAGLAYK
28.0743	10	XVARXPSGVK
28.0745	10	LVEIXTEMEK
28.0746	10	LLNWXMQIAK
28.0824	11	HMLWKAGILYK
28.0825	11	HVLWKAGILYK
28.0826	11	SMLPETTVVRR
28.0827	11	SVLPETTVVRR
28.0828	11	GMDNSVVLSRK
28.0829	11	GVDNSVVLSRK
28.0830	11	GTFNSVVLSRK
28.0369	9	GLAXHQLXA
1259.02	9	DTVDTVLEK
1259.10	9	PVTIGECPK
1259.14	10	FTAVGKEFNK
1259.16	11	RTLDFHDSNVK
1259.21	11	KTRPILSPLTK
1259.26	11	GTHPSSSAGLK
1259.28	11	ILWILDRLFFK
1259.29	9	WILDRLFFK
1259.30	11	CTYRRFKYGLK
1259.31	9	KSMRHEYRK
1259.33	9	YIQMCTELK
1259.37	10	MVMELVRMIK
1259.38	9	VMELVRMIK
1259.41	11	LIRPNENPAHK
26.0023	8	VSPGVWIR
26.0024	8	VSPGWTHK

5

10

15

20

25

30

35

PEPTIDE	AA	SEQUENCE
26.0026	8	ASFCGGSPY
26.0035	9	TSPYELSLY
26.0036	9	TSIPFLHEY
26.0041	9	FNDPGPGTY
26.0045	9	YVDLGLALRY
26.0051	9	DADRSFIEY
26.0055	9	NMDKAVKLY
26.0056	9	TTDNFYRNY
26.0058	9	HSAEALQKY
26.0059	9	LTAGLDFAY
26.0061	9	LTYKYNQFY
26.0062	9	CSNDKSLVY
26.0063	9	RSARASSRY
26.0065	9	ASADKPYSY
26.0067	9	STTAGPNEY
26.0069	9	LSGNNGHFHY
26.0073	9	NTFVQANLY
26.0074	9	GTATYLPPY
26.0081	9	RLDAFRQTY
26.0082	9	KAEVHTFYY
26.0083	9	VAEGDTVIY
26.0084	9	LTEIDIRDY
26.0085	9	HTEFEGQVY
26.0086	9	VSDGGPNLY
26.0092	9	IIEDQYNRY
26.0093	9	FLDQWWTEY
26.0095	9	FVEDPQNGKY
26.0096	9	ISDESYRVY
26.0156	9	YLAEDADLSY
26.0197	9	ALLAVGATK
26.0198	9	ALNFPQGSQK
26.0199	9	AVGATKVPR
26.0203	9	FSVSVSQLR
26.0204	9	GTATLRLVK
26.0205	9	GVSQQLRTK
26.0207	9	LIYRRRLMK
26.0211	9	OLVLHQILK

5

10

15

20

25

30

35

PEPTIDE	AA	SEQUENCE
26.0212	9	SSHWLRLPR
26.0214	9	TMEVTVYHR
26.0216	9	VLASLIYRR
26.0217	9	VSCQGGLPK
26.0218	9	VVLASLIYR
26.0227	9	GTQCALTRR
26.0251	9	FTIPYWDWR
26.0252	9	GTPEGPLRR
26.0253	9	KSYLEQASR
26.0255	9	LVSLLCRHK
26.0256	9	MVPFIPLYR
26.0258	9	QTSAGHFPR
26.0259	9	SIFEQWLRR
26.0260	9	SLLCRHKRK
26.0261	9	SSWQIVCSR
26.0267	10	NMQJGGVLTY
26.0273	10	RMAQNFAMRY
26.0274	10	FTVQGSLSGY
26.0275	10	QTSPYELSLY
26.0276	10	SSNAILSLSY
26.0280	10	TSQPWWPADY
26.0284	10	VSDVSIIPY
26.0285	10	ASDAQSANKY
26.0286	10	FTETNLAGEY
26.0287	10	YVDGFEPNGY
26.0291	10	FNDPGPGTYY
26.0296	10	FLDQWWTEYY
26.0299	10	AAEFATETAY
26.0309	10	NAEVVLNQLY
26.0311	10	FVDGDSLFEY
26.0316	10	PSEDAQVAVY
26.0317	10	MSDNIRTGLY
26.0318	10	ESELREILNY
26.0319	10	CMESVRNGTY
26.0320	10	KTENGITRLY
26.0321	10	LTEIDIRDYY
26.0397	10	LLVLMMAVVA

5

10

15

20

25

PEPTIDE	AA	SEQUENCE
26.0424	10	AVVLASLIYR
26.0425	10	GALLAVGATK
26.0426	10	GTATLRLVKR
26.0427	10	HTMEVTVYHR
26.0428	10	IALNFPGSQK
26.0432	10	QLRALDGGNK
26.0433	10	QVPLDCVLYR
26.0434	10	SLIYRRRLMK
26.0435	10	SSSHWLRLPR
26.0438	10	TVSCQGGLPK
26.0442	10	VVLASLIYRR
26.0466	10	YVKVLUHHTLK
26.0473	10	LIGCWYCRRR
26.0474	10	LLIGCWYCRR
26.0485	10	SSMHNALHIY
26.0504	10	CVSSKNLMEK
26.0510	10	FSSWQIVCSR
26.0511	10	GLVSLLCRHK
26.0518	10	YMVPFIPLYR
26.0535	11	GVWIRTPPAYR
26.0539	11	RLVVDFSQFSR
26.0545	11	TLPETTVVRRR
26.0549	11	LLPIFFCLWVY
	11	STLPETTVVRR
26.0550	11	RAFPHCLAFSY

Table 9

Sequence	AA	Strain	Stage	No.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
ALRKGQEL	9	1			15	2.1		<0.0003			
ILESLFRAV	9	1			93	2.1		0.0004			
VITKVKADL	9	1			101	2.1		<0.0003			
CLGLSYDGL	9	1/3			174	2.1		0.0004			
QIMPKTKFL	9	1			187	2.1		0.0007			
SLHCKPPEAL	10	1			7	2.1		0.0002			
PLVLTGLEV	10	1			37	2.1		0.0008			
CILESLFRAV	10	1			92	2.1		0.0003			
AVITKVKADL	10	1			100	2.1		0			
VITKVKADLV	10	1			101	2.1		0			
LLKRYRAREPV	10	1/3			114	2.1		0			
EIPKQASSEL	10	1			142	2.1		0			
CLGLSYDGLL	10	1/3			174	2.1		0			
ALSRKVKVEL	9	2			101	2.1		0.0003			
KMVELVHFL	9	2			105	2.1		0.16			
HVELVHPLL	9	2			106	2.1		0.0031			
DLQQLSLRVL	9	2			143	2.1		0			
SLRVLAAGL	9	2			147	2.1		0.0001			
ALSRKVKVEL	9	3			101	2.1		0.0050			
HLY1PATCL	9	3			167	2.1		0.0003			
YIPATCLGL	9	3			169	2.1		0.018			
QIMPKAGLL	9	3			187	2.1		0			

Sequence	AA	Mass Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AISRKMKVELV	10	2		101	2.1		0			
MVBLYHFLLL	10	2		106	2.1		0.0017			
KLPGLLSRDL	10	2		135	2.1		0			
LLSRDLQQSL	10	2		139	2.1		0.0007			
SLPTTMYPL	10	3		63	2.1		0.0035			
DLSBSPFQAL	10	3		93	2.1		0.0001			
ALSRKVAVLV	10	3		101	2.1		0.0001			
KVABLVHPLL	10	3		105	2.1		0.012			
VIFSKASSL	10	3		142	2.1		0			
SLQLVPGIEL	10	3		150	2.1		0.0049			
LMEVDPIGHL	10	3		159	2.1		0.0005			
FLIVLVMI	9	1		194	2.1		0.0005			
GLLGDNQIM	9	1		181	2.1		0.0051			
SLHCKPERA	9	1		7	2.1		0.013	<0.0002	0	
ALALVVCVQA	9	1		22	2.1		0.015	<0.0002	<0.0002	
CKPERALEA	9	1		10	Random		<0.0002			
QQEALGLVC	9	1		19	Random		<0.0002			
VQATSSBS	9	1		28	Random		<0.0002			
PLVLTLEE	9	1		37	Random		<0.0002			
VPTAGSTD	9	1		46	Random		<0.0002			
PQSPQGASA	9	1		55	Random		<0.0002			
PPTINPTR	9	1		64	Random		<0.0002			

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QRPQEGSS	9	1		73	Random		<0.0002			
SREBGPST	9	1		82	Random		<0.0002			
AVITKVKAD	9	1		100	Random		<0.0002			
EMLESVIKN	9	1		127	Random		<0.0002		0	
YKICPPBIV	9	1		136	Random		<0.0002			
QKASSESIQL	9	1		145	Random		<0.0002			
VFGIDVKEA	9	1		154	Random		<0.0002	<0.0002	0	
DPTGHSTYV	9	1		163	Random		<0.0002			
VTGJGLSYD	9	1		172	Random		<0.0002			
PKTGFLIV	9	1		190	Random		<0.0002			
LVMIAEAGG	9	1		199	Random		<0.0002			
HAPBEEINE	9	1		208	Random		<0.0002			
ELSGVREVID	9	1		217	Random		<0.0002			
GREHSAYGE	9	1		226	Random		<0.0002			
PRKLUTQDL	9	1		235	Random		0.0002			
VQEKYLBYG	9	1		244	Random		<0.0002			
RCRTVIPHA	9	1		253	Random		<0.0002			
MSSCCGVQGP	9	1		262	Random		<0.0002			
ILESLSPRAVI	10	1		93	2.1		0.0002			
PLIIVLVMIA	10	1		194	2.1		0.0003	0.0093	0.0030	
LVFGIDVKEA	10	1		153	2.1		0.0002	<0.0002	0	
EVIIDGREHSA	10	1		222	2.1		0	<0.0002	0	

Sequence	AA	Mass Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GVQGSPSIKPA	10	1		266	2.1			0.0001		
QIVPGIDV	8	1		152	2.1			0		
KLITQDLV	8	1		237	2.1			0.0004		
GLLGDNGI	8	1		181	2.1			0		
DLYQFLL	8	1		108	2.1			0		
GLSXKDKL	8	1		176	2.1			0.0001		
DLYQEKYL	8	1		242	2.1			0		
LLQDNQIM	8	1		182	2.1			0		
PLIIVLVM	8	1		194	2.1			0		
ALRQQEA	8	1		15	2.1			0		
TLEEVPTA	8	1		42	2.1			0		
IMPCTGFL	8	1		188	2.1			0.0001		
PTTQAEML	8	1		122	2.1			0		
IVLVMIAN	8	1		197	2.1			0.0001		
AVITKVA	8	1		100	2.1			0		
EIWBBSLV	8	1		213	2.1			0		
LIVLVVMI	8	1		195	2.1			0.0001		
LIVLVVIA	8	1		196	2.1			0.0002		
SIFRAVITKRV	11	1		96	2.1			0.0001		
LLKRYRAREPV	11	1		113	2.1			0.0001		
YLBYGRCRTVI	11	1		248	2.1			0.0006		
ALRQQEALQL	11	1		15	2.1			0.0001		

Sequence	AA	Mass Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PLIVVJMIAM	11	1		194	2.1			0.0041		
VLGTLBEVPTA	11	1		39	2.1			0.0002		
QLVFGIDVKEA	11	1		152	2.1			0.0001		
AVITKKVADLV	11	1		100	2.1			0		
PVTKABMLBSV	11	1		122	2.1			0		
KVADLVGVFLLL	11	1		105	2.1			0.020		
GVQGSPSLKPAN	11	1		266	2.1			0		
LVGFLLLKYRA	11	1		109	2.1			0.0004		
LVMIAAMEGGHA	11	1		199	2.1			0.0005		
CILESILPRAVI	11	1		92	2.1			0.0030		
RALRQQEA	9	1		14	2.1			0	<0.0002	0
EAQQBEAQL	9	1		17	2.1			0		<0.0002
AATSSSSPL	9	1		30	2.1			0		<0.0002
ATSSSSPLV	9	1		31	2.1			0.0007		
GTLEBEVPTA	9	1		41	2.1			0.013	<0.0002	0
GAGAPPTI	9	1		60	2.1			0		<0.0002
STSCILSLSL	9	1		89	2.1			0.0002		
RAVITKKVVA	9	1		99	2.1			0	<0.0002	0
ITKKVADLV	9	1		102	2.1			0		
RAREPVTKA	9	1		118	2.1			0		
KAEMBBSVI	9	1		125	2.1			0		<0.0002
KASEBSLQLV	9	1		146	2.1			0.0009		

Sequence	AA	Wage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PTGHSYVIV	9	1		164	2.1		0			
KTGFPLIIVL	9	1		191	2.1	0.006				
LIIVLVVIA	9	1		195	2.1	0	0.0022	0.0006		
IIVLVVIAAM	9	1		196	2.1	0.007				
MIAMEGGA	9	1		201	2.1	0.005	<0.0002	0.0002		
EIWEELSVM	9	1		213	2.1	0				
SAYGEPRKL	9	1		230	2.1	0.002			<0.0002	
YLEYGRCRT	9	1		248	2.1	0				
BALGLVVCVQA	10	1		21	2.1	0.0005	<0.0002	0		
QAATSSSSPL	10	1		29	2.1	0			<0.0002	
VTKAEMLBSV	10	1		123	2.1	0				
EADPTGHSIV	10	1		161	2.1	0				
VLGTLREEVPT	10	1		39	2.1	0.0004				
SAFPPTINFT	10	1		62	2.1	0				
GIDVKBEADPT	10	1		156	2.1	0				
PTGHSYVLT	10	1		164	2.1	0				
FLWGPRALA	9	1	new	265	2.1	0.042	0.0017	0		
LAETSYVKV	9	1	new	272	2.1	0				
YVKVLEYVIL	9	1	new	277	2.1	0.0002				
RVRFFPPSL	9	1	new	290	2.1	0.0001				
LAETSYVKVL	10	1	new	272	2.1	0				
VLEYVIKVSA	10	1	new	280	2.1	0.0002	0.0002	0		

Sequence	AA	Mass Strain	Mol.	Pos.	Notif	A1	A2.1	A3.2	A11	A24
ANLREEREGV	10	1	new	301	2.1		0			
SMHCKPBBV	9	1	new (a)	7	2.1		0.018			
AMGLVCVQV	9	1	new (a)	22	2.1		0.012			
LMLGTLBBV	9	1	new (a)	38	2.1		0.13			
LQLVFGIDV	9	1	new	151	2.1		0.0004			
GLSYDGLG	9	1	new	176	2.1		0			
GLSYDGLV	9	1	new (a)	176	2.1		0.0047			
LLDQNQIMP	9	1	new	182	2.1		0.0001			
LLDQNQIMV	9	1	new (a)	182	2.1		0.043			
WEEISVMEV	9	1	new	215	2.1		0			
WEEISVMEV	9	1	new (a)	215	2.1		0.041			
RKJJTQDLV	9	1	new	236	2.1		0			
YEPFLWGPRV	9	1	new	262	2.1		0			
AATSSSSPLV	10	1	new	30	2.1		0			
ATSSSSPLV	10	1	new	31	2.1		0			
KMADLYGFLV	10	1	new (a)	105	2.1		1.5			
VADLYGPLL	10	1	new	106	2.1		0.0008			0.0003
SESIQLVFGI	10	1	new	148	2.1		0			
VMVTCUGLSV	10	1	new (a)	170	2.1		0.30			
QIMPKNGPLI	10	1	new	187	2.1		0.0009			
QMPKNGFLV	10	1	new (a)	187	2.1		0.050			

Sequence	AA	Wage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KTQFLLIVV	10	1	new	191	2.1				0.0012	
LIVLVVIAN	10	1	new	195	2.1				0.0003	
VMIAAMBGGHV	10	1	new (a)	200	2.1				0.053	
SAYGBPRKLL	10	1	new	230	2.1		0		0.0008	
ALAETSYVKVL	11	1 N		270	2.1		0.012			
KMVELVHPLLL	11	2		52	2.1		0.67			
ELMEVDPIGHL	11	3		105	2.1		0.026			
HLYIPATCLQL	11	3		114	2.1		0.041			
LLLKYKRAAREPV	11	3		60	2.1		0.0001			
QLVPGIBLMEV	11	3		99	2.1		0.34			
IMPKAGILLIV	11	3		135	2.1		0.013			
VLYTCLGLSYDGL	13	1 n	B6	170	2.1		0.0017			
KLTQDLYQEKYL	13	1 n	B6	237	2.1		0.0060			
DLVQBKYLYRQV	13	1 n	B6	242	2.1		0			
SLPRAVITKKVADLV	15	1 n	POL	96	2.1		0.0004			
DLESEBFQAAISRQMV	15	2	POL	40	2.1		0			
MLGSVVGNTMQYFFPV	15	3	POL	75	2.1		0.012			
GASSFSTTI	9	2		60	2.1		0		0.0002	
DLESEBFQAA	9	2,3		93	2.1		0			
QAAISRQMV	9	2		99	2.1		0			
KARMLBSVL	9	2		125	2.1		0			0
KASSEVILQLV	9	2		146	2.1		0.011			

Sequence	AA	Mass Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QIVTGIEKV	9	2		152	2.1		0.0038			
VVPIISHLYI	9	2		162	2.1		0.0002			
PISHLYILV	9	2		164	2.1		0.0005			
HLVILVTCL	9	2		167	2.1		0.0034			
YILVTCLGL	9	2		169	2.1		0.0014			
GLLGADNQVM	9	2		181	2.1		0.0038			
QVMPKTRILL	9	2		187	2.1	0	0.230			
VMPKTELLI	9	2		188	2.1		0.0010			
KTGLLIVL	9	2		191	2.1		0.0002			
GLLIVLAI	9	2,3		193	2.1		0.0002			
LLIVLVAII	9	2,3		194	2.1		0.0001			
LIVLVAIA	9	2,3		195	2.1		0.0008			
IIVLVAII	9	2		196	2.1		0.0009			
IIAIEGDCA	9	2		201	2.1	0	0.0010			
GASSLPTTM	9	3		60	2.1	0	0			
QAALSRKVA	9	3		99	2.1	0	0			
VAEVLVHPLL	9	3		106	2.1	0	0.039			
KAEMLGSSV	9	3		125	2.1	0				
KASSSLQLV	9	3		146	2.1		0.0005			
QLVPGIFLM	9	3		152	2.1		0.0010			
PIGHLYIPA	9	3		164	2.1	0				
IMPKAGLLI	9	3		188	2.1		0.0064			

Sequence	AA	Wage	Strain	Mol.	Pos.	Notiz	A1	A2.1	A3.2	A11	A24
KAGLLIVL	9	3		191	2.1			0.0002			0
IIARBGDCA	9	3		201	2.1			0			
BALEAQGEAL	10	1	new	14	2.1			0		0	
EAQQRALGLV	10	1	new	17	2.1			0			
DLESEPPQAI	10	2		93	2.1			0			
AAISRQMTL	10	2		100	2.1			0		0	
VIPSKASGYL	10	2		142	2.1			0.0014			
YIQLVFGIEV	10	2		150	2.1			0.37			
LVPGEIEWV	10	2		153	2.1			0.018			
GIEVEVWVPI	10	2		156	2.1			<0.0002			
WVEVPISHL	10	2		159	2.1			<0.0002			
EVVPISHLYI	10	2		161	2.1			<0.0002			
WVPISHLYIL	10	2		162	2.1			0.0002			
PISHLYILV	10	2		164	2.1			0.0003			
QVMPKTLII	10	2		187	2.1			0.0002			
VMPKTLII	10	2		188	2.1			0.0009			
KTGLLIVLVA	10	2		191	2.1			<0.0002			
GLLIVLVAII	10	2,3		193	2.1			0.0005			
LLIVLVAIA	10	2,3		194	2.1			<0.0002			
LIIVLVAIAI	10	2		195	2.1			0.0013			
AIIAIAGDCA	10	2		200	2.1			0.0023			
AALSRKVAVL	10	3		100	2.1			0.0007		0	

Sequence	AA	Wage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VAELVHPLL	10	3		106	2.1		0.059			0.0018
VTKAEMLGSV	10	3		123	2.1		<0.0002			
GIELMEVDPI	10	3		156	2.1		<0.0002			
EVDPIGHLYI	10	3		161	2.1		<0.0002			
PIGHLYIPAT	10	3		164	2.1		0.0003			
QIMPKAGLLI	10	3		187	2.1		0.0006			
IMPKAGLLII	10	3		188	2.1		0.0015			
KAGLLIIVLA	10	3		191	2.1		<0.0002			
AIARERGDCA	10	3		200	2.1		<0.0002			
PLNGSPRALI	9	2		271	A02					
GLERARGRAL	9	3		15	A02					
EARGEALGL	9	3		17	A02					
ALGLVGAQA	9	3		22	A02/A03					
GLVGAQAPA	9	3		24	A02/A03					
LYGAQAPAT	9	3		25	A02					
PATEEQEAA	9	3		31	A02/A03					
EAASSSSSTL	9	3		37	A02					
AAASSSSSTLV	9	3		38	A02					
LVEVTIGEV	9	3		45	A02					
EVTIGEVPA	9	3		47	A02/A03					
VTIGEVPA	9	3		48	A02/A03					
KIWEELSVL	9	3		220	A02					

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
SILGDPKKL	9	3		237	A02					
ILGDPKKL	9	3		238	A02					
PLNGPRALV	9	3		271	A02					
RALVETSYV	9	3		276	A02					
LVEETSYVKV	9	3		278	A02					
YVKVLUHHEV	9	3		283	A02					
KVLHHMKVKI	9	3		285	A02					
RARGRALGLV	10	3		17	A02					
EAQGLVTAQAA	10	3		21	A02/A03					
GLVTAQAAQAPAT	10	3		24	A02					
QAPATEEQQA	10	3		29	A02/A03					
EAASSSESTLV	10	3		37	A02					
TLVVEVTLAEV	10	3		44	A02					
EVTLGDEVPA	10	3		47	A02/A03					
EVFEGREDSI	10	3		229	A02					
SILGDPKKLL	10	3		237	A02					
ILGDPKKLIT	10	3		238	A02					
ALVETSYVKV	10	3		277	A02					
LVEETSYVKV	10	3		278	A02					
MVKISGGPHI	10	3		290	A02					
LVLGTLR&EV	9	1		38	2.1	<0.0006	0.032	0	0	0.0003
KVADLWGPFL	10	1		105		0.0005	0.041	0.0039	0.0030	0.0070

Sequence	AA	Major Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
LVFGIETMEV	10	3		153	2.1		0.17			
ILLWQPIPV	9	3			<0.0007	1.4	0.0048	0.0048	0	
EVDPIGHLY	9	3				3.7			0.0022	
KAVELVHPL	9	2			<0.0007	0.13	0.0007	0	0.0043	
KAVELVHFL	10	2		105		<0.0008	0.071	0.0004	0.0001	0.0008
LVFGIETMEV	10	3			0.0030	0.065	0.0007	0	0	
KVAFLVHPL	9	3		105	2.1	0	0.073	0.011	0.0047	0.0005
CILSSLPRA	9	1		92	2.1	0.0001	0.073	0	0.0002	0
VMIAAMEGGHA	10	1		200	2.1	<0.00008	0.0023	0	0	0
MLESVIKEY	10	1				0	0	0.034	0.0045	0
ETSYKVKLEY	10	1			0.075	0	0.0009	0.0004	0	
KYLEVIKV	9	1	new	279	2.1	<0.0005	0.095	0.022	0.015	0
PLNGPRAA	9	1			<0.0006	0.027	0.0015	0	0	
ALRBBBEGV	9	1		302	2.1	<0.0006	0.0056	0	0	0
ALAETSYKV	10	1		271		<0.0007	0.017	0.0011	0.0029	0
YVIVNSARV	9	1		283	2.1	0.0005	0.018	0	0	0
RALAETSYV	9	1		270	2.1	<0.0006	0.014	0.0003	0.0005	0
ALAETSYKV	9	1			<0.0006	0.0002	0.17	0.39	0	
VIGTLBEGV	8	1		39	2.1	<0.0007	0.0088	0	0	0
SLQAVFGI	8	1		150	2.1	<0.0007	0.0094	0	0.0001	0
IILSSLPRA	8	1		93	2.1	<0.0004	0.0017	0.0003	0	0.0001
PLLLKYRA	8	1		112	2.1	0.0036	0.0007	0.0003	0.0001	0

Sequence	Mass Strain	Mol.	Pos.	Notif	A1	A2.1	A3.2	A11	A24
GLVCVQAA	9	1		24	2.1	0.0016	0.0008	0	0
VLYTCLGL	9	1		170	2.1	<0.0007	0.0010	0	0
KVADLVGPL	9	1		105	2.1	<0.0008	0.0091	0.0013	0.0005
YVLVTCGLL	9	1		169	2.1				
IMPKTQPLI	9	1		188	2.1	<0.0008	0.0035	0	0
GLLQDNQIM	9	1			A2.1	<0.0008	0.0054	0	0.0002
GLVCVQAAAT	9	1		24	2.1	0.0030	0.0007	0.0026	0
VADLVGPL	9	1		106	2.1	0.032	0.0011	0.0054	0.0008
YLYKGRCRTV	10	1		248	2.1	0.0008	0.0097	0.0001	0
SQLQVFGIDV	10	1		150	2.1	0.0028	0.0047	0.0013	0.0001
IMPKNGFLII	10	1		188	2.1	<0.0008	0.0007	0	0.050
ALGLVCVQAA	10	1		22	A2.1	0.0011	0.0002	0.0003	0
EIWERLSVMEV	11	1		213	A2.1	0.0007	0.013	0.0001	0
FLIVLVLWLM	11	1			A2.1	0.023	0.0031	0.016	0.0014
VIPIHAMSSCGV	11	1		257	2.1	<0.0009	1.4	0	0
CILESCFRAVI	11	1			A2.1	0.079	0.0017	0.058	0.0005
QIMPKTQPLII	11	1		187	2.1	<0.0009	0.0003	0	0.0030
QFLLLKYPKA	9	1						0.0004	0.0002
CPPBIPGKWA	9	1						0	0
PPPPSGLREA	9	1						0	0
PPPSLREAA	9	1						0	0
RSLHCKPBEA	10	1						0.0001	0.0008

Sequence	AA	Mass strain	Mol.	Pos.	Notif.	A1	A2.1	A3.2	A11	A24
EFLWGPRLAA	10	1						0	0	
RFFPSLREA	10	1						0.0004	0	
PPPPSLRBA	10	1						0	0	

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max. Binding
						Binding	Binding	Binding	Binding	Binding	
ALFLGFLGAA	HIV	MN	gp160	518	A02	0.4950					0.4950
MLQLTVWGI	HIV	MN	gp160	566	A02	0.2450					0.2450
RVIEVLQRA	HIV	MN	gp160	829	A02	0.1963					0.1963
KLTPLCVTL	HIV	MN	gp160	120	A02	0.1601					0.1601
LLIAARIVEL	HIV	MN	gp160	776	A02	0.1550					0.1550
SLLNATDIAV	HIV	MN	gp160	814	A02	0.1050					0.1050
ALFLGFLGAA	HIV	MN	gp160	518	A02	0.0945					0.0945
HMLQLTVWGI	HIV	MN	gp160	565	A02	0.01677					0.01677
LLNATDIAV	HIV	MN	gp160	815	A02	0.01617					0.01617
ALLYKLDIV	HIV	MN	gp160	179	A02	0.01362					0.01362
WLWYIKIFI	HIV	MN	gp160	679	A02	0.01355					0.01355
TIVVHLNESV	HIV	MN	gp160	288	A02	0.01350					0.01350
LLOQYWSQEL	HIV	MN	gp160	800	A02	0.01265					0.01265
IMIVGGLVGL	HIV	MN	gp160	687	A02	0.01252					0.01252
LLYKLDIVSI	HIV	MN	gp160	180	A02	0.01245					0.01245
FLAIIWVDL	HIV	MN	gp160	753	A02	0.01233					0.01233
TLQCKIKQII	HIV	MN	gp160	415	A02	0.01200					0.01200
GLVGLRIVFA	HIV	MN	gp160	692	A02	0.01195					0.01195
FLGAAGSTM	HIV	MN	gp160	523	A02	0.01190					0.01190
IISLWDQSL	HIV	MN	gp160	107	A02	0.01179					0.01179
TVWGIKQLOA	HIV	MN	gp160	570	A02	0.01150					0.01150
LLGRRGWEV	HIV	MN	gp160	785	A02	0.01142					0.01142
AVLSIVNRV	HIV	MN	gp160	701	A02	0.01132					0.01132

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max. Binding
FIMIVGGGLV	HIV	MN	gp160	686	A02	0.0131					0.0131
LLNATDIAVA	HIV	MN	gp160	815	A02	0.0117					0.0117
FLYGALLLA	PLP	Human		80	A02		1.9000				1.9000
SLLTFMIAA	PLP	Human		253	A02		0.5310				0.5310
FMIATATYNFAV	PLP	Human		257	A02	0.4950					0.4950
RMYGVLPW1	PLP	Human		205	A02		0.1650				0.1650
IAATYNFAV	PLP	Human		259	A02		0.0540				0.0540
QLECCARCLV	PLP	Human		2	A02		0.0515				0.0515
YALTVVWLL	PLP	Human		157	A02		0.0415				0.0415
ALTVVWLLV	PLP	Human		158	A02		0.0390				0.0390
FLYGALLL	PLP	Human		80	A02		0.0345				0.0345
SLCADARMYGV	PLP	Human		199	A02		0.0140				0.0140
LLVFACSAV	PLP	Human		164	A02		0.0107				0.0107

Table 10

AA	SEQUENCE	SOURCE
9	YIFATCLGL	MAGE 3 169
9	IMPKTGFLI	MAGE 1 188
10	IMPKTGFLII	MAGE 1 188
15	MLGSVVGWNWQYFFPV	MAGE 3 POL 75
9	VMPKTGLLI	MAGE 2 188
9	IMPKAGLLI	MAGE 3 188
10	IMPKAGLLII	MAGE 3 188
9	RLWHYPCTV	HCV Env2 614
9	RLWHYPCTI	HCV Env2 614
9	FLLLADARI	HCV Env2 -
9	GVWPILLLL	HCV Env2 792
15	GMWPILLLL	HCV Env2 792
9	YLNTPGLPV	HCV NS3/NS4 1542
9	YMNTPGLPV	HCV NS3/NS4 1542
9	VILDSFDPL	HCV NSS 2251
9	ILMTHFFSI	HCV NSS 2843
20	ILMTHFFSV	HCV NSS 2843
9	LMAVVLASL	gp100 606
9	SLSLGFLFL	PAP 13
10	YMIMVKCWM	c-ErbB2 952
10	GLHGQDLFGI	PAP 196
9	AILSVSSFL	P. falciparum CSP 6
25	GLIMVLSFL	P. falciparum CSP 425
9	VLLGGVGLV	P. falciparum EXP-1 91
9	GLLGNVSTV	P. falciparum EXP-1 83
9	LLGNVSTVL	P. falciparum EXP-1 84
30	VLAGLLGNV	P. falciparum EXP-1 80

AA	SEQUENCE	SOURCE
9	KILSVFFLA	<i>P. falciparum</i> EXP-1 2
9	FLIFFDLFL	<i>P. falciparum</i> TRAP 14
9	LIFFDLFLV	<i>P. falciparum</i> TRAP 15
9	FMKAVCVEV	<i>P. falciparum</i> TRAP 230
5	LLMDCSGSI	<i>P. falciparum</i> TRAP 51
10	ILSVSSFLFV	<i>P. falciparum</i> CSP 7
10	VLLGGVGLVL	<i>P. falciparum</i> EXP-1 91
10	GLLGNVSTVL	<i>P. falciparum</i> EXP-1 83
10	FLIFFDLFLV	<i>P. falciparum</i> TRAP 14
10	GLALLACAGL	<i>P. falciparum</i> TRAP 507
9	KIWEELSML	MAGE2 220
9	TLMSAMTNL	Prost.Ca PAP 112
9	LLLARAASL	Prost.Ca PAP 6
9	ALDVYNGLL	Prost.Ca PAP 299
15	VTWIGAAPL	PSA 8
10	ALIETSYVKV	MAGE2 277
10	SLSLGFLFL	Prost.Ca PAP 13
10	RTLMSAMTNL	PAP 111
20	FLPSDFFPSV(CONH2)	HBc 18-27
10	FLPSDFFPSV-NH2	HBc 18-27
9	ILGFVFVTL-NH2	Flu Matrix 59-67
10	KGILGFVFVTL-NH2	Flu Matrix 57-66
11	FLPSDFFPSVR	HBc 18-28
9	FLPSDFFPS	HBc 18-26
25	GILGKVFTL	Flu Matrix 58-66 analog
9	FLSKQYLN	HBV polymerase
9	KLQCVPLHV	PSA 166-174 P/D

AA	SEQUENCE	SOURCE
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
9	KLYEIVAKV	A2.1 consensus
9	KLAEYVAKV	A2.1 consensus
9	KLAEIVYKV	A2.1 consensus
9	TLTSCNTSV	HIV gp 120 env. RE trans. 197
9	ALMEKIYQV	A2.1 consensus peptide
9	ALSEKIYQV	A2.1 consensus peptide
9	FLMSYFPSV	941.01 9-mer analog
9	FLPSYFPSV	941.01 9-mer analog
10	FLMSDYFPSV	941.01 M2 analog
9	FLCYFALV	Chiron consensus
9	FMYCYFALV	Chiron consensus
10	SLVGPGILCV	Chiron consensus
15	SLMGCGGLFWV	Chiron consensus
8	GLLGPLLV	HBVadr-ENV
9	AMAKAAAAI	A2.1 poly-A
10	MMWYWGPSLY	HBV
9	FLPSYFPSA	analog of 994.02: chiron comb
20	FAPSYFPSV	analog of 994.02: chiron comb
9	FLPSYFPSS	analog of 994.02: chiron comb
9	FSPSYFPSV	analog of 994.02: chiron comb
9	IMPKTGFLI	MAGE-1
9	VADLVGFLL	MAGE-1
25	EIWEELSVMEV	MAGE-1
11	FLITVLVMIAM	MAGE-1
11	VIPHAMSSCGV	MAGE-1
11	CILESCFRAVI	MAGE-1
9	YIFATCLGL	MAGE3

5

10

15

20

25

30

AA	SEQUENCE	SOURCE
9	YIFATCLGL	MAGE3
11	KMVELVVHFL	MAGE2 112-122
11	HLFIYATCLGL	MAGE3 174-184
9	GLQDCTMLV	HCV NSS 2727-2735
8	TLGIVSPI	HPV, analog of 1088.01
8	TLGIVXPI	HPV, analog of 1088.01
10	FLLAQFTSAI	HBV POL 513
11	VLLDYQGMLPV	HBV env
11	CILLCLIFLL	HBV env
9	FLGGSPVCL	HBV env
11	TVIEYLVSFGV	HBV core 114-124
11	TVLEYLVSFGV	HBV core 114-124
10	FLLAQFTSAI	HBV pol
9	GLYSSTVPI	HBV pol
9	GLYSSTAPI	HBV pol
9	GLDVLTAKV	HIV form VIN.
9	RILGAVAKV	HIV form VIN.
9	LLFGYPVYV	HTLV, tax 11-19
9	ALFGYPVYV	tax 11-19, SAAS
9	LLFGAPVYV	tax 11-19, SAAS
9	LLFGYAVYV	tax 11-19, SAAS
9	LLFGYPVAV	tax 11-19, SAAS
9	AAGIGILT	MART1 27-35
9	GILT	MART1 31-39
9	ILTV	MART1 32-40
9	VILGV	MART1 35-43
9	ALMDKSLHV	MART1 56-64
10	TVILGV	MART1
10	LLDG	MART1
10	ILSVSSPLFV	Plas. falcip. CSA-A 7-16
9	GLIMVLSFL	Plas. falcip. CSA-A 401-409

5

10

15

20

25

30

AA	SEQUENCE	SOURCE
9	IMVLSFLFL	Plas. falcip. CSA-A 403-411
10	FLIFFDLFLV	Plas. falcip. TRAP-A 14-23
9	FMKAVCDEV	Plas. falcip. TRAP-A 200-207
9	IMPGQEAGL	gp100
9	GLGQVPLIV	gp100
9	LMAVVLASL	gp100
9	RLMKQDFSV	gp100
9	HLAVIGALL	gp100
9	LLAVGATKV	gp100
9	MLGTHTMEV	gp100
10	LLDGTATLRL	gp100
10	VLYRYGSFSV	gp100
10	VLPSPACQLV	gp100
10	SLADTNNSLAV	gp100
10	VLMAVVLASL	gp100
10	LMAVVLASLI	gp100
10	RLDCWRGGQV	gp100
10	AMLGTHITMEV	gp100
10	ALDGGNKHFL	gp100
9	YLEPGPVTA	gp100
10	LLNATAIAAVA	
11	SLLNATAIAAVA	
9	KTWGQYWQV	gp100
9	ITDQVPPSV	gp100
9	YLEPGPVTA	gp100
10	LLDGTATLRL	gp100
10	VLYRYGSFSV	gp100
10	ALDGGNKHFL	gp100
9	GILTVILGV	MART1 31-39
9	YMNGTMSQV	Human Tyrosinase
9	MLLAVLYBL	Human Tyrosinase
9	LLWSFQTSA	Human Tyrosinase

5

10

15

20

25

AA	SEQUENCE	SOURCE
9	YLTLAKHTI	Human Tyrosinase
9	FLPWHRLFL	Human Tyrosinase
9	FLLRWEQEI	Human Tyrosinase
9	RIWSWLLGA	Human Tyrosinase
9	LLGAAMVGA	Human Tyrosinase
9	AMVGAVLTA	Human Tyrosinase
9	VLTALLAGL	Human Tyrosinase
9	ALLAGLVSL	Human Tyrosinase
9	LLAGLVSSL	Human Tyrosinase
10	BLLWSFQTS	Human Tyrosinase
10	WMHYYVSMDA	Human Tyrosinase
10	FLPWHRLFLL	Human Tyrosinase
10	WLLGAAMVGA	Human Tyrosinase
10	AMVGAVLTA	Human Tyrosinase
10	VLTALLAGLV	Human Tyrosinase
10	TALLAGLVSL	Human Tyrosinase
10	ALLAGLVSSL	Human Tyrosinase
9	NLTDALLQV	<i>P. falciparum</i> SSP2 132
9	SAWENVKNV	<i>P. falciparum</i> SSP2 218
10	FLIFFDLFLV	<i>P. falciparum</i> SSP2 14
9	NLNDNAIHL	<i>P. falciparum</i> SSP2 80
10	YLLMDCSGSI	<i>P. falciparum</i> SSP2 51
9	TLQDVSLLEV	controls

Table 11

5

10

15

20

25

AA	SEQUENCE	SOURCE
9	ALYWFRGI	HPV 6b/11 E1 319
	LLDGNPMSI	HPV 6b/11 E1 540
9	NAWGMVLLV	HPV 6b/11 E1 270
9	SLYAHIQWL	HPV 6b/11 E1 260
9	TLIKCPPLL	HPV 6b/11 E1 556
9	GIYDALFDI	PSMAg 707
9	YLSGANLNL	CEA 605
9	VLYGPDTPI	CEA 589
9	IMIGVLVGV	CEA 691
9	LLTFWNPPT	CEA 24
9	KLTEMVQWA	HPV 6b/11 E1 357
9	YMDTYMRNL	HPV 6b/11 E1 532
10	NLLDGNPMSI	HPV 6b/11 E1 539
10	SLYAHIQWLT	HPV 6b/11 E1 260
10	TLIKCPPLLV	HPV 6b/11 E1 556
10	MVFELANSIV	PSMAg 583
10	YLWWVNNQSL	CEA 176
10	YLWWVNNQSL	CEA 354
10	YLWWVNGQSL	CEA 532
10	GIMIGVLVGV	CEA 690
10	VLYGPDAPI	CEA 233
10	KLIEPLSLYA	HPV 6b/11 E1 254
10	WLCAGALVLA	PSMAg 20
10	IMIGVLVGVVA	CEA 691

5

10

15

20

AA	SEQUENCE	SOURCE
9	YLYQLSPPI	HTLV-I tax 155
9	LLFEEYTNI	HTLV-I tax 307
9	QLGAFLTNV	HTLV-I tax 178
9	TLTAWQNGL	HTLV-I tax 226
9	ALQFLIPRL	HTLV-I tax 67
9	TLGQHLPTL	HTLV-I tax 123
9	FAFKDLFVV	HPV 18 E6 47
9	RLLQLLFRA	GCDFP-15 2
9	CMVVKTYLI	GCDFP-15 65
9	LLLVLCLQL	GCDFP-15 15
9	ILYAHIQCL	HPV18 E1 266
9	SLACSWGMV	HPV16 E1 266
9	CLYLHIQSL	HPV16 E1 259
9	YLVSPLSDI	HPV16 E1 90
9	VMFLRYQGV	HPV16 E1 443
9	KLLSKLLCV	HPV16 E1 292
9	ALDGNPISI	HPV18 E1 546
9	AVFKDTYGL	HPV18 E1 216
9	LLTTNIHPA	HPV18 E1 570
9	LLQQYCLYL	HPV16 E1 254

AA	SEQUENCE	SOURCE
9	AMLAKFKEL	HPV16 E1 206
9	ALDGNLVSM	HPV16 E1 539
9	FLGALKSFL	HPV18 E1 463
9	FIHFIQGAV	HPV18 E1 497
10	TLLLVLCLQL	GCDFP-15 14
10	LLFRASPATL	GCDFP-15 6
10	SLMKFLQGSV	HPV16 E1 489
10	SLACSWGMVV	HPV16 E1 266
10	FLQGSVICFV	HPV16 E1 493
10	FIQGAVISFV	HPV18 E1 500
10	KLLCVSPMCM	HPV16 E1 296
10	FILYAHIQCL	HPV18 E1 265
10	FVNSTSHFWL	HPV18 E1 508
10	ILLTTNIHPA	HPV18 E1 569
10	TLLQQYCLYL	HPV16 E1 253
9	GLLGWSPQA	HBV ENV 62
9	GLACHQLCA	HER2/neu
9	ILDEAYVMA	HER2/neu
9	SIISAVVGI	HER2/neu
9	VVLGVVFGI	HER2/neu
9	YMIMVKCWM	HER2/neu
10	ALCRWGLLA	HER2/neu
10	QLFEDNYALA	HER2/neu

5

10

15

20

AA	SEQUENCE	SOURCE
9	HMWNFISGI	HCV consensus
9	VIYQYMDDL	HIV POL 358
9	SLYNTVATL	HIV GAG 77
10	TVWGIKQLQA	HIV ENV 73S
9	LLEAGALV	MSH 99
9	VLETAVGLL	MSH 92
9	CLALSDLLV	MSH 79
9	FLSLGLVSL	MSH 45
9	SLVENALVV	MSH 52
10	AIIDPLIYA	MSH 291
9	FLCWGPFFL	MSH 251
9	FLALIICNA	MSH 283
9	TILLGIFFL	MSH 244
9	RLLGSLNST	MSH 9
15	SLYNTVATL	HIV p17/5B 77-8
9	VIYQYMDDL	HIV RT/50A 346-
9	ILKEPVHGV	HIV RT/IV9 476-

Table 12

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
1237.01	9	FLWGPQALV
1237.02	9	FLWGPNALV
1237.03	9	FLWGPHALV
1237.04	9	FLWGPKALV
1237.05	9	FLWGPFFALV
26.0158	9	AVIGALLAV
26.0172	9	LLHLAVIGA
26.0186	9	SLADTNSLA
26.0192	9	VMGTTLAEM
26.0240	9	LLAVLYCLL
26.0383	10	FLRNQPLTFA
26.0390	10	HLAVIGALLA
26.0395	10	LAVIGALLAV
26.0418	10	TLAEMSTPEA
26.0423	10	YLAEADLSYT
26.0497	10	MILLAVLYCLL
1183.10	10	VLYRYGSFSV
27.0007	9	ILSSLGLPV
27.0012	9	LLFLGVVFL
27.0019	9	GLYGAQYDV
27.0022	9	FVVALIPLV
27.0023	9	GLMTAVYLV
27.0027	9	ALVLLMLPV
27.0028	9	ILLSIARVV
27.0029	9	SLYFGGICV
27.0030	9	QLIPCMDVV
27.0031	9	VHQOSTYQL
27.0032	9	AHNVVHAI
27.0034	9	GLHGVGVSV
27.0035	9	GLVDFVKHI
27.0036	9	LLFRFMRPL
27.0038	9	LMLPGMNGI
27.0043	9	TVLRFVPPL
27.0044	9	MLGNAPSVV
27.0050	9	YLDLALMSV
27.0064	9	RMPEAAPPV

5

10

15

20

25

30

35

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
27.0082	9	FLLPDAQSI
27.0083	9	MTYAAPLFV
27.0088	9	LLPLGYPFV
27.0089	9	GLYYLTTEV
27.0090	9	MALLRLPLV
27.0091	9	RLPLVLPAV
27.0093	9	RMFAANLGV
27.0095	9	RLLDDTPEV
27.0096	9	YLYVHSPAL
27.0100	9	GLYLSQIAV
27.0101	9	YLSQIAVLL
27.0102	9	SLAGFVRML
27.0137	10	ATYDKGILTV
27.0146	10	KIFMLVTAVV
27.0151	10	FLLADERVRV
27.0153	10	MLATDLSLRV
27.0154	10	RLQPQVGWEV
27.0161	10	FLMPVEDVFI
27.0165	10	RMSRVTTFTV
27.0168	10	LALVLLMLPV
27.0169	10	ALVLLMLPVV
27.0170	10	GIVSGILLSI
27.0171	10	SLYFGGICVI
27.0173	10	QLIPCMDVVL
27.0181	10	LLFRFRMRPLI
27.0183	10	VLLEDGGVEV
27.0184	10	AMPAYNWMTV
27.0186	10	GLAGTVLRFV
27.0188	10	VLIAFGRFPI
27.0189	10	FLTC DANLAV
27.0197	10	AIAWGAWGEV
27.0204	10	LLLETSWEAI
27.0217	10	RMPEAAPPVA
27.0223	10	WMAETTLGRV
27.0226	10	AMALLRLPLV
27.0229	10	FMSLAGFVRM
27.0266	11	SLLTEVETYVL

5

10

15

20

25

30

35

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
27.0268	11	GILGFVFTLTV
27.0269	11	VLDVGDAYFSV
27.0271	11	KIWEELSMLEV
27.0272	11	STLVEVTLGEV
27.0273	11	GLAPPOHLIRV
27.0274	11	HLIRVEGNLRV
27.0005	9	YLLALRYLA
27.0013	9	GLYRQWALA
27.0017	9	LLWQDPVPA
27.0040	9	ALLSDWLPA
27.0045	9	WLLIDTSNA
27.0046	9	MLASTLTDAA
27.0081	9	YLSEGDMAA
27.0094	9	LLACAVIHA
27.0144	10	LLCCSGVATA
27.0191	10	LLATVFKLTA
27.0192	10	KLTADGVITA
27.0195	10	GLGGIQLFFA
28.0064	8	TLGIVXPPI
28.0065	8	ALGTTXYA
28.0293	9	FLLTRILTV
28.0294	9	ALMPLYACV
28.0295	9	LLAQFTSAV
28.0296	9	LLPFVQWFV
28.0297	9	FLLAQFTSV
28.0298	9	KLHLYSHPV
28.0299	9	KLFLYSHPI
28.0300	9	LLSSNLSWV
28.0301	9	FLLSLGIHV
28.0302	9	MMWYWGPSV
28.0303	9	VLQAGFFLV
28.0304	9	PLLPIFFCV
28.0305	9	FLLPIFFCL
28.0306	9	VLLDYQGMV
28.0307	9	YMDDVVVLGV
28.0308	9	YMFDVVLGA
28.0309	9	GLLGWSPQV

5

10

15

20

25

30

35

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
28.0342	9	YMIMVKXWM
28.0343	9	YIFATXLGL
28.0345	9	SLHXXKPEEA
28.0346	9	ALGLVXVQA
28.0348	9	LLMDXSGSI
28.0349	9	FAFRDLXIV
28.0352	9	GTLGIVXPI
28.0353	9	TLGIVXPIX
28.0354	9	LLWFHISXL
28.0355	9	KLTPLXVTL
28.0356	9	ALVEIXTEM
28.0357	9	LTFGWXFKL
28.0359	9	KLQXVDLHV
28.0360	9	FMKAVXVEV
28.0361	9	LLQQYXLYL
28.0362	9	XLYLHIQSL
28.0363	9	SLAXSWGMV
28.0364	9	ILYAHIQXL
28.0365	9	KLLSKLLXV
28.0366	9	PLLPIFFXL
28.0367	9	TLIKXPPLL
28.0368	9	ALMPLYAXI
28.0370	9	XILESILFRA
28.0609	10	FLLAQFTSAV
28.0610	10	YLHTLWKAGV
28.0611	10	YLFTLWKAGI
28.0612	10	YLLTLWKAGI
28.0613	10	LLFYQQMLPV
28.0614	10	LLLYQQMLPV
28.0615	10	LLVLQAGFFV
28.0616	10	ILLLCLIFLV
28.0650	10	ALXRWGLLL
28.0651	10	KLPDLXTEL
28.0652	10	HLYQQGXQVV
28.0653	10	XILESILFRA
28.0654	10	KLQXVDLHV
28.0655	10	YIFATXLGL

5

10

15

20

25

30

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
F111.01	9	SLYNTVATL
F111.02	9	ALYNTVATL
F111.04	9	SLANTVATL
F111.06	9	SLFNAVATL
F111.07	9	SLFNLLATL
F111.10	9	SLFNTIAVL
F111.11	9	SLFNAVAVL
F111.09	9	SLFNTIVVL
F111.12	9	SLFNAIAVL
F111.13	9	SLFNTVAVL
F111.14	9	SLFNTVCVI
F111.15	9	SLHNTVATL
F111.17	9	SLHNTVAVL
F111.18	9	SLYATVATL
F111.19	9	SLYNAVATL
F111.21	9	SLYNTAATL
F111.22	9	SLYNTIAVL
F111.23	9	SLYNTSATL
F111.25	9	SLYNTVAVL
F111.26	9	SLYNTVATA
F111.27	9	SLYNIAITL
F111.28	9	SLYNLVAVL
F111.29	9	SLFNLLAVL
F111.32	9	SLFNTVVTL
F111.34	9	SLYNTVAAL
1039.031	9	MMWYWGPSL
1211.40	10	SLLNATAIAV
	10	TIHDIILECV
	9	FAFRDLCIV
	9	GTLGIVCPI
	9	TLGIVCPIC

Table 13

A A	SEQUENCE	SOURCE
5	9 IPQSLDSWW	HBV ENV 191
10	9 IPIPSSWAF	HBV ENV 313
15	9 TPARVTGGV	HBV POL 365
	9 LPIFFCLWV	HBV ENV 379
	9 HPAAMPHLL	HBV POL 440
	9 FPHCLAFSY	HBV POL 541
	9 DPSRGRLGL	HBV POL 789
	9 QPRGRRQPI	HCV Core 57
	9 SPRGSRPSW	HCV Core 99
	9 DPRRRSRNL	HCV Core 111
	9 LPGCSFSIF	HCV Core 168
	9 YPCTVNFTI	HCV E2 622
	9 LPALSTGLI	HCV E2 681
	9 HPNIEEVAL	HCV NS3 1358
	9 SPGALVVGV	HCV NS4 1887

5

10

15

20

A	SEQUENCE	SOURCE
A		
9	SPGQRVEFL	HCV NSS 2615
9	APTLWARMI	HCV NSS 2835
9	FPRIWLHJL	HIV VPR 34
9	SPTRRELQV	HIV POL 37
9	FPVRPQVPL	HIV NEF 84
9	RPQVPLRPM	HIV NEF 87
9	KPCVKLTPL	HIV ENV 123
9	SPRTLNAWV	HIV GAG 153
9	FPISPIETV	HIV POL 171
9	SPAIFQSSM	HIV POL 327
9	NPDIVIYQY	HIV POL 346
9	GPGHKARVL	HIV GAG 360
9	LPEKDSWTV	HIV POL 417
9	YPLASLRSL	HIV GAG 507
9	VPRRKAKII	HIV POL 991
9	TPTLHEYML	HPV16 E7 5
9	KPLNPAEKL	HPV18 E6 110
9	NPAEKLRLH	HPV18 E6 113
9	VPISHLYIL	MAGE2 170
9	MPKTGLLII	MAGE2 196

5

10

15

A A	SEQUENCE	SOURCE
9	DPACYEFLW	MAGE2 265
9	EPHISYPPL	MAGE2 296
9	YPPLHERAL	MAGE2 301
9	LPTTMNYPL	MAGE3 71
9	DPIGHLYIF	MAGE3 170
9	MPKAGLLII	MAGE3 196
9	GPHISYPPL	MAGE3 296
9	HPSDGKCNL	P. falciparum S
9	RPRGDNFAV	P. falciparum S
9	QPRPRGDNF	P. falciparum S
9	LPNDKSDRY	P. falciparum S
10	LPLDKGIKPY	HBV POL 123
10	TPARVTGGVF	HBV POL 365
10	FPHCLAFSYM	HBV POL 541
10	LPRRGPRLGV	HCV Core 37
10.	APLGGAARAL	HCV Core 142
10	LPGCSFSIFL	HCV Core 168
10	VPASQVCGPV	HCV E2 497
10	YPCTVNFTIF	HCV E2 622

5

10

15

A	SEQUENCE	SOURCE
A		
10	SPLLLSTTEW	HCV E2 663
10	RPSGMFDSSV	HCV NS3 1506
10	LPVCQDHLEF	HCV NS3 1547
10	KPTLHGPTPL	HCV NS3 1614
10	TPLLYRLGAV	HCV NS3 1621
10	NPAIASLMAF	HCV NS4 1783
10	LPAILSPGAL	HCV NS4 1882
10	SPGALVVGVV	HCV NS4 1887
10	APTLWARMIL	HCV NS5 2835
10	IPVGEIYKRW	HIV GAG 261
10	YPLASLRSLF	HIV GAG 507
10	APTKAKRRVV	HIV ENV 547
10	VPISHLYILV	MAGE2 170
10	MPKTGLLIIV	MAGE2 196
10	HPRKLLMQDL	MAGE2 241
10	LPTTMNYPLW	MAGE3 71
10	MPKAGLLIIV	MAGE3 196

A A	SEQUENCE	SOURCE
10	IPYSPLSPKV	P. falciparum S
10	TPYAGEPAPF	P. falciparum S
9	FPDHQLDPA	HBV ENV 14
9	YPALMPLYA	HBV POL 640
9	LPVCAFSSA	HBV X 58
9	APLGGAAARA	HCV 142
9	DPTTPLARA	HCV 2806
9	FPYLVAYQA	HCV 1582
9	LPAILSPGA	HCV 1882
9	NPAIASLMA	HCV 1783
9	TPIDTTIMA	HCV 2551
9	TPLLYRLGA	HCV 1621
9	WPLLLLLLA	HCV 793
9	NPYNTPVFA	HIV POL 225
9	APLLLARAA	PAP 4
9	HPQWVLTAA	PSA 52
10	IPIPSSWAFA	HBV ENV 313
10	TPPAYRPPNA	HBV NUC 128
10	APFTQCGYPA	HBV POL 633
10	LPIHTAELLA	HBV POL 712
10	GPCALRFTSA	HBV X 67

A	SEQUENCE	SOURCE
A		
10	DPTTPLARAA	HCV 2806
10	IPQAVVDMVA	HCV 339
10	LPCSFITLPA	HCV 674
10	QPEKGGRKPA	HCV 2567
10	VPHPNIEEVA	HCV 1356
10	IPAETGQETA	HIV POL 820
10	LPQGWKGSPA	HIV POL 320
10	FPDLESEFQA	MAGE2/3 98
10	DPIGHLYIFA	MAGE3 170
9	EPLSLYAH1	HPV 6b/11 E1 2
9	PPLLVTSNI	HPV 6b/11 E1 5
9	SPRLDAIKL	HPV 6b/11 E1 1
9	TPKKNCIAI	HPV 6b/11 E1 4
9	FPFDRNGNA	HPV 6b/11 E1 5
10	CPPLLVTSNI	HPV 6b/11 E1 5
10	FPFDRNGNAV	HPV 6b/11 E1 5
8	GPLVLQAA	HBV ENV 173
8	IPIPSSWA	HBV ENV 313

A	SEQUENCE	SOURCE
A		
8	VPFVQWFV	HBV ENV 340
8	LPIFFCLW	HBV ENV 379
8	RPPNAPIL	HBV NUC 133
8	MPLSYQHF	HBV POL 1
8	HPAAMPHL	HBV POL 429
8	SPFLLAQF	HBV POL 511
8	YPALMPLY	HBV POL 640
8	SPTYKAFL	HBV POL 659
8	VPSALNPA	HBV POL 769
8	HPvhAGPI	HIV con. GAG
8	GPGvRyPL	HIV con. NEF
8	SPIETVPV	HIV con. POL
8	NPYNTPVF	HIV con. POL
8	LPIQKETW	HIV con. POL

5

10

15

A A	SEQUENCE	SOURCE
8	VPRRKaKi	HIV con. POL
8	VpLQLPPI	HIV con. REV
8	VPLAMKLI	P. falciparum
8	LPYGRRTL	P. falciparum
8	RPRGDNFA	P. falciparum
8	IPQQEPNI	P. falciparum
8	TPFAGEPA	P. falciparum
9	SPINTIAEA	HPV 6b E1 93
9	SPISNVANA	HPV 11 E1 93
9	SPRLDAIKL	HPV 6b/11 E1 1
9	EPLSLYAH	HPV 6b/11 E1 2
9	EPPKIQSGV	HPV 6b/11 E1 3
9	IPFLTKFKL	HPV 6b E1 455
9	TPKKNCIAI	HPV 6b/11 E1 4
9	QPLTDKVA	HPV 11 E1 512
9	PPLLVTSNI	HPV 6b/11 E1 5

5

10

15

20

25

A A	SEQUENCE	SOURCE
9	FPFDRNGNA	HPV 6b/11 E1 5
9	APLILSRIV	PSA 14
9	HPEDTGQVF	PSA 78
9	HPLYDMSLL	PSA 94
9	HPQKVTKFM	PSA 184
9	GPLVCNGVL	PSA 211
9	RPSLYTKVV	PSA 235
9	FPPEGVSIW	PAP 124
9	NPILLWQPI	PAP 133
9	LPFRNCPRF	PAP 156
9	IPSYKKLIM	PAP 277
9	LPPYASCHL	PAP 307
9	SPSCPLERF	PAP 348
9	CPLERFAEL	PAP 351
9	GPTLIGANA	gp100 74
9	LPDGQVIWV	gp100 97
9	VPLAHSSSA	gp100 198
9	QPLTFALQL	gp100 236
9	DPSGYLAEA	gp100 246
9	EPGPVTAQV	gp100 282
9	MPTAESTGM	gp100 366
9	TPAEVSIVV	gp100 401
9	LPKEACMEI	gp100 520
9	LPSPACQLV	gp100 545
9	VPLIVGILL	gp100 596
9	LPHSSSHWL	gp100 630

A	SEQUENCE	SOURCE
A		
9	CPIGENSPL	gp100 647
9	SPLLSGQQV	gp100 653
9	MPREDAHFI	MART1 1
9	APLGPQFPF	Tyrosinase 6
9	IPIGTYGQM	Tyrosinase 1
9	TPMFNDINI	Tyrosinase 1
9	LPWHRLFLL	Tyrosinase 2
9	IPYWDWRDA	Tyrosinase 2
9	SPASFFSSW	Tyrosinase 2
9	LPSSADVEF	Tyrosinase 3
9	SPLTGIADA	Tyrosinase 3
9	DPIFLLHHA	Tyrosinase 3
9	IPLYRNGDF	Tyrosinase 4
9	YPELPKPSI	CEA 141
9	LPVSPRLQL	CEA 185
9	LPVSPRLQL	CEA 363
9	NPPAQYSWL	CEA 442
9	LPVSPRLQL	CEA 541
9	IPQQHTQVL	CEA 632
9	NPPAQYSWF	CEA 264
9	LPSIPVHPI	Prost.Ca PSM
9	IPVHPIGYY	Prost.Ca PSM
9	RPFYRHVIY	Prost.Ca PSM
9	TPKHNMKAF	Prost.Ca PSM
9	FPGIYDALF	Prost.Ca PSM
9	RPRWLCAGA	Prost.Ca PSM
9	DPLTPGYPA	Prost.Ca PSM

A	SEQUENCE	SOURCE
A		
9	RPRRTILFA	Prost.Ca PSM
9	LPFDCRDYA	Prost.Ca PSM
9	LPIHTAELL	HBV POL 712
10	GPDADTISPL	CEA 236
10	IPQQHTQVLF	CEA 632
10	QPIPVHTVPL	Prost.Ca PAP
10	HPYKDFIATL	Prost.Ca PAP
10	LPGCSPSCPL	Prost.Ca PAP
10	LPSWATEDTM	Prost.Ca PAP
10	VPLSEDQLLY	Prost.Ca PAP
10	FPHPLYDMSL	Prost.Ca PSA
10	RPGDDSSHDL	Prost.Ca PSA
10	HPQKVTKFML	Prost.Ca PSA
10	LPFDCRDYAV	Prost.Ca PSM
10	YPNKTHPNYI	Prost.Ca PSM
10	SPEFSGMPRI	Prost.Ca PSM
10	RPRWLCAGAL	Prost.Ca PSM
10	TPKHNMK AFL	Prost.Ca PSM
10	RPFYRHVIYA	Prost.Ca PSM
20	HPAAMPHLLV	HBV POL 429
9	SPREGPLPA	HER2/neu 1151
9	KPDLSYMPI	HER2/neu 605
9	HPPPAFSPA	HER2/neu 1208

A	SEQUENCE	SOURCE
A		
9	GPLPAARPA	HER2/neu 1155
9	APQPHPPPAA	HER2/neu 1204
9	EPLTPSGAM	HER2/neu 698
9	LPTHDPSP	HER2/neu 1101
9	DPLNNNTPV	HER2/neu 121
9	SPLTSIISA	HER2/neu 649
9	SPKANKEIL	HER2/neu 760
9	LPTNASLSF	HER2/neu 65
9	CPSGVKPDL	HER2/neu 600
10	SPLAPSEGA	HER2/neu 1073
9	MPNQAQMRI	HER2/neu 706
9	LPAARPAGA	HER2/neu 1157
9	LPQPICTI	HER2/neu 941
9	SPAFDNLYY	HER2/neu 1214

5

10

A A	SEQUENCE	SOURCE
9	TPTAENPEY	HER2/neu 1240
9	LPSETDGYV	HER2/neu 1120
10	LPTNASLSFL	HER2/neu 65
10	CPAEQRASPL	HER2/neu 642
10	KPCARVCYGL	HER2/neu 336
10	APQPHPPPAF	HER2/neu 1204
10	SPGGLRELQL	HER2/neu 133
10	SPLTSIISAV	HER2/neu 649
10	MPNQAQMRIL	HER2/neu 706
10	SPYVSRLLG1	HER2/neu 779
10	HPPPAFSPA1	HER2/neu 1208
10	SPREGPLPAA	HER2/neu 1151
10	NPHQALLHTA	HER2/neu 488
10	MPYGCLLDHV	HER2/neu 801

5

10

A A	SEQUENCE	SOURCE
10	GPASPLDSTF	HER2/neu 995
9	LPTTLFQPV	HTLV-I tax 21
9	IPPSFLQAM	HTLV-I tax 10
9	FPGFGQSLL	HTLV-I tax 4
9	WPLLPHVIF	HTLV-I tax 16
9	SPPITWPLL	HTLV-I tax 16
9	VPYKRIEEL	HTLV-I tax 18
9	RPQNLYT LW	HTLV-I tax 13
9	CPKDGQPSL	HTLV-I tax 26
9	RPNDEVTAV	GCDFP-15 47
9	SPATLLLVL	GCDFP-15 11
9	WPYLNRLV	HPV16 E1 576
9	QPFILYAH	HPV18 E1 263
9	SPRLKAIC	HPV16 E1 107

A	SEQUENCE	SOURCE
A		
9	SPLGERLEV	HPV18 E1 97
9	SPRLQEISL	HPV18 E1 110
9	RPIVQFLRY	HPV18 E1 447
10	WPYLHNRLVV	HPV16 E1 576
5	WPYLESRITV	HPV18 E1 583
10	QPPKLRSSVA	HPV18 E1 315
10	EPPKLRSTAA	HPV16 E1 308
9	DPSRGRLGL	HBV POL 778
9	HPAAMPHLL	HBV POL 429
10	IPIPSSWAF	HBV ENV 313
10	TPARVTGGVF	HBV POL 354
10	FPHCLAFSYM	HBV POL 530
9	LPVCAFSSA	HBV X 58
9	YPALMPLYA	HBV POL 640
15	APLLLARAA	PAP 4

A A	SEQUENCE	SOURCE
9	HPQWVLTAA	PSA 52
9	HPSDGKCNL	Pf SSP2 206
9	RPRGDNFAV	Pf SSP2 305
9	QPRPRGDNF	Pf SSP2 303
10	TPYAGEPAPF	Pf SSP2 539
9	GPHISYPPL	MAGE3 296
9	YPPLHERAL	MAGE2 301
9	VPISHLYIL	MAGE2 170
9	EPHISYPPL	MAGE2 296
9	LPTTMNYPL	MAGE3 71
9	MPKAGLLII	MAGE3 196
10	HPRKLLMQDL	MAGE2 241

Table 14

PEPTIDE	AA	SEQUENCE
25.0129	9	LPPLERLTL
26.0445	10	EPGPVTAQVV
26.0448	10	LPRIFCSCPI
26.0449	10	LPSPACQLVL
26.0455	10	VPLAHSSSAF
26.0458	10	VPRNQDWLGV
26.0476	10	APPAYEKLSA
26.0478	10	MPREDAHFIY
26.0519	10	APAFLPWHRL
26.0522	10	GPNCTERRLL
26.0523	10	IPLYRNGDFF
26.0529	10	TPRLPSSADV
19.0101	9	TPAEVSIVV
26.0554	11	APFTQCGYPAL
26.0561	11	NPADDPSRGRL
26.0564	11	RPPNAPILSTL
26.0566	11	SPFLLAQFTSA
26.0567	11	SPHHTALRQAI
26.0568	11	TPARVTGGVFL

WHAT IS CLAIMED IS:

1. A composition comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14 or a peptide comprising a conservative substitution of a residue in a peptide shown in Table 3-14.
5
2. The composition of claim 1, wherein the immunogenic peptide is linked to a second oligopeptide.
- 10 3. The composition of claim 2, wherein the second oligopeptide is a peptide that induces a helper T response.
- 15 4. A composition comprising a nucleic acid molecule encoding an immunogenic peptide as shown in Tables 3-14, or a peptide comprising a conservative substitution of a residue of a peptide shown in Table 3-14.
5. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding a second immunogenic peptide.
- 20 6. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding an oligopeptide that induces a helper T response.
7. A method of inducing a cytotoxic T cell response comprising contacting a cytotoxic T cell with a peptide of claim 1.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : A61K 39/00, 39/29; C07K 7/00, 14/02, 14/82
US CL : 424/185.1; 530/300, 328, 350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/185.1; 530/300, 328, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
STN file=reg of first sequence in Table 3. Examiner's MHC/peptide files.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN file=reg sequence search of first sequence in Table 3. STN file=ca of hits on sequence search.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	BRUSS, V. A short linear sequence in the pre-S domain of the large hepatitis B virus envelope protein required from virion formation. J. Virology. December 1997, Vol. 71, No. 12, pages 9350-9357. See entire document	1-3 and 7
Y	PREISLER-ADAMS, S. et al. Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identification of three types of C open reading frame. Nucleic Acids Res. 1993, Vol. 21, No. 9, page 2258. See entire document.	1-3 and 7
Y	RAMMENSEE, H. et al. Peptides naturally presented by MHC Class I molecules. Annu. Rev. Immunol. 1993, Vol. 11, pages 213-243, see entire article.	1-3 and 7

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	*T*	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
B earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 12 MAY 1998	Date of mailing of the international search report 17 JUL 1998
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer THOMAS CUNNINGHAM Telephone No. (703) 308-0196
Facsimile No. (703) 305-3230	<i>Jab</i> <i>for</i>

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/05039

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ENGELHARD, V. et al. Structure of peptides associated with MHC Class I molecules. Curr. Opin. Immunol. 1994, Vol. 6, pages 13-23, see entire document.	1-3 and 7

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/05039

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See attached sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-3 and 7

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/05039

Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

1. This International Search Authority has found 3453 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-3 and 7, drawn to compositions comprising peptides and methods of inducing CTL responses using such compositions. A review of Tables 3-14 indicates there are 2764 structurally different peptides recited.

Group II, claim(s) 4-6, drawn to nucleic acids encoding peptides. Claims 4-6 recite nucleic acids encoding the 2764 different peptides of Tables 3-14.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. The species are as follows:

Each of the 2764 different peptides recited by Tables 3-14 and each of the 2764 different nucleic acid sequences encoding the peptides of Tables 3-14. $2764 + 2764 = 5,528$ total species.

The claims are deemed to correspond to the species listed above in the following manner:

The following claims are generic: claims 1-7 because they encompass all of the peptides or nucleic acid sequences encoding the peptides of Tables 3-14.

The first peptide species recited in Table 3 (FTP. . .LSK) will be examined. Each additional peptide species requires the payment of a separate fee. To have all the recited peptide species searched requires the payment of 2763 additional fees.

Upon payment for Group II, the Office will examine the first ten (or ten that the Applicant selects) nucleic acid species at no additional cost. Each four species of nucleic acids thereafter requires the payment of a separate fee. To have all the nucleic acid species searched requires the payment of $(2764-10)/4 = 689$ additional fees.

and it considers that the International Application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below:

The inventions listed as Groups I and II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the peptides of Group I lack the corresponding technical structural and functional features of the nucleic acids of Group II.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: the 5528 different species of peptides recited by Tables 3-14 (or the nucleic acid sequences encoding such peptides) lack the same or corresponding special technical features of common structure and function, source of isolation and amino acid or nucleic acid identity. Each separate species would require a separate prior art search.